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M protein: protein search, using sw model

Run on: July 12, 2002, 14:41:47 / Search time 15.83 seconds

(with alignments)
569,909 million cell updates/sec

Hit list: US-08-826-361a-4

Sequence: 1 VLLILHAEHPHVLISPSA.....CRNVVYDILLKMLNAHL 234

Search filter: R1:SDM62
Gapop 10.0 / Gapext 0.5

Searchset: 107224 steps, 48719550 residues

Total number of hits satisfying chosen parameters: 107224

Minimum hit seq length: 0

Maximum hit seq length: 200000000

Post processing: Minimum Match 0%

Maximum Match 100%

Listed first 45 summaries

Database: SwissProt_40*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being plotted, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Query Match Length DB	ID	Description
1	1181	100.0	540 1	Q92731 homo sapien
2	1169	99.0	279 1	ESR2_HUMAN
3	1165	98.1	527 1	ESR2_SHEEP
4	1141	95.8	527 1	ESR2_BOVIN
5	1111	94.1	540 1	ESR2_PAT
6	1105	93.6	540 1	ESR2_CAVIA
7	1103.5	93.4	546 1	ESR2_PIG
8	1103	93.4	540 1	ESR2_MOUSE
9	1062	89.9	541	ESR2_STIMU
10	1058	89.6	472 1	ESR2_CHICK
11	1056	89.4	472 1	ESR2_GALLA
12	862	70.4	410 1	ESR2_CAVIA
13	840	70.3	572 1	ESR2_ARENA
14	828	69.7	575 1	ESR2_PIG
15	826	69.4	568 1	ESR1_CAVIA
16	820	69.4	568 1	ESR2_CAVIA
17	809	68.5	559 1	ESR2_SPANU
18	797	67.5	557 1	ESR2_PIG
19	796	67.3	474 1	ESR2_MOUSE
20	791	67.0	545 1	ESR1_MOUSE
21	771	65.3	569 1	ESR1_CHICK
22	768	65.0	587 1	ESR1_PIG
23	759	64.3	595 1	ESR1_HUMAN
24	756	64.0	599 1	ESR1_MOUSE
25	753	63.8	595 1	ESR1_PIG
26	750	63.5	600 1	ESR1_PAT
27	749	63.4	595 1	ESR1_MOUSE
28	745.5	63.1	525 1	ESR1_MOUSE
29	738.5	62.5	585 1	ESR1_MOUSE
30	735	62.2	449 1	ESR1_ARENA
31	714	62.2	566 1	ESR1_XERHA
32	713	61.9	594 1	ESR1_MOUSE
33	701.5	61.9	561 1	ESR1_PIG

34	700.5	61.9	620 1	ESR1_ORVIA
35	728.5	61.7	579 1	ESR1_SPANU
36	718	60.8	588 1	ESR1_MOUSE
37	708.5	60.0	622 1	ESR1_MOUSE
38	708	59.9	569 1	ESR1_MOUSE
39	704.5	59.7	535 1	ESR1_SALSA
40	697	59.0	617 1	ESR1_MOUSE
41	643	54.4	407 1	ESR1_MOUSE
42	553.5	46.9	174 1	ESR1_MOUSE
43	365	30.9	458 1	ESR1_HUMAN
44	358	30.4	433 1	ESR2_PAT
45	358	30.3	500 1	ESR2_HUMAN

ALIGNMENTS

RESULT 1

ID ESR2_HUMAN STANDARD: P01: 540 AA

AC Q92731, 660685, 669638, 667584, 660702, 660703, 660584, 660685

AC Q90966, Q90903

DI 15-JUL-1999 (Ref. 48, created)

DI 15-JUL-1999 (Ref. 48, last sequence update)

DI 16-OCT-2001 (Ref. 49, last annotation update)

DE Estrogen receptor beta (ER-beta)

GN ESR2 OR NR3A2 OR ESRRB

OS Homo sapiens (human)

OC Eukaryota; Euteleostomi; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID=9606

LN

RP SEQUENCE FROM N.A. (ISOPFORM BETA-1).

RX MEDLINE-98139878; PubMed 9474491

RA Osawa S., Inoue S., Watanabe T., Hiroi H., Orimo A., Hosoi T., Ouchi Y., Muramatsu M.

RT "The complete primary structure of human estrogen receptor beta (hER-beta) and its heterodimerization with ER-alpha in vivo and in vitro."

RT Biochem. Biophys. Res. Commun. 244:122-126(1998).

RL

LN

RP SEQUENCE FROM N.A. AND ALTERNATIVE SPLICING.

RX MEDLINE-96354875; PubMed 8766414

RA Mosselman S., Polman J., Di Roma P., "ER beta: identification and characterization of a novel human estrogen receptor."

RT FEBS Lett. 392:49-53(1996).

RL

LN

RP SEQUENCE FROM N.A. (ISOPFORM BETA-2/3), AND CHARACTERIZATION.

RX MEDLINE-98379282; PubMed 9671811

RA Osawa S., Inoue S., Watanabe T., Orimo A., Hosoi T., Ouchi Y., Muramatsu M.

RT "Molecular cloning and characterization of human estrogen receptor beta cDNA: a potential inhibitor of estrogen action in human."

RT Nucleic Acids Res. 26:4945-4952(1998).

RL

LN

RP SEQUENCE OF 59-510 FROM N.A. (ISOPFORM BETA-5A AND BETA-6).

RX MEDLINE-98379282; PubMed 9671811

RA Brundage A.W., Lohrke D., Taylor R.N., Jaffe R.B., Schaffner A. (1996) "The ER-beta gene and its expression in human."

RL

LN

RP SEQUENCE FROM N.A. (ISOPFORM BETA-2A).

[illegible]

RESULT	3
ID	PSR2_SHEEP
STANDARD:	PRT: 527 AA.
AC	Q90115; Q90116;
DT	16-OCT-2001 (rel. 40), created)
DI	16-OCT-2001 (rel. 40), last sequence update)
D1	16-OCT-2001 (rel. 40), last annotation update)
DE	Esteroid receptor beta (ER-beta).
CN	PSR2 OR NR3A2.
OS	Ovis aries (Sheep).
OC	Eukaryota, Metazoa, Chordata, Vertebrata, Euteleostomi,
NC	Mammalia, Eutheria, Artiodactyla, Ruminantia, Bovidae, Boviformes,
OX	Bovidae, Caprinae, Ovis.
NP	NPII_taxid:9440;
RN	[1]
RP	SEQUENCE FROM N.A. (ISOFORMS BETA AND BETA-1).
RS	TISSUE-SPECIFIC:
RA	Gardneras H., Healy K.M., Figg W.P., Reflow K.P.,
PT	"Isolated rat estrogen receptor beta from the ovine
RL	ovary."
HL	Submitted (Aug 1999) to the EMBL/GenBank/DDBJ databases.
CC	1. FORMED BY TWO INTERGINS WITH AN AFFINITY SIMILAR TO THAT OF
CC	EN ALPHA, AND ACTIVATES EXPRESSION OF SUBSTRATE GENES CONTAINING
CC	ESTEROID RECEPTOR ELEMENTS (ERE). IN AN INTERGIST DIFFERENT MANNER.
CC	1. SUBUNIT BINDS DNA AS A HOMODIMER, CAN FORM A HETERODIMER WITH ER
CC	ALPHA (BY SIMILARITY).
CC	-1. SUBCELLULAR LOCATION: Nuclear.
CC	-1. ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS; BETA (SHOWN HERE) AND
CC	BETA-1 ARE PRODUCED BY ALTERNATIVE SPLICING.
CC	-1. DOMAIN: COMPOSED OF THREE DOMAINS: A MOTILATING N-TERMINAL DOMAIN
CC	A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
CC	1. SIMILARITY: RELATED TO THE NUCLEAR RECEPTOR FAMILY.
CC	NR3 SUPERFAMILY.
CC	..
CC	This SWISS-PROT entry is copyright. It is produced through a collation
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation
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CC	use by non-profit institutions as long as its content is to be combined
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CC	activities requires a license agreement (see http://www.ebi.ac.uk/cdd/
CC	or send an email to license@sb.scri.ch).
CC	..
D8	EMBL: AF177946; AAC55772.1; ..
D8	EMBL: AF257109; AAF71745.1; ..
D8	HSSP: P03872; IHC1.
D8	InterPro: IPRO00586; Hormone_rec_fam.
D8	InterPro: IPRO01728; Steroid_hormone_receptor.
D8	InterPro: IPRO01628; Z1-C4.
D8	Planr: PR00104; hormone_rec_1.
D8	Prims: PR00105; z1-c4; 1.
D8	PRINTS: PR00348; SIKHOBM_NBR.
D8	PRINTS: PR00047; SIROBFINDR.
D8	SMART: SM00430; BOLL1; 1.
D8	SMART: SM00499; ZNF_C4; 1.
D8	PROSITE: PS00931; NOVEL_ER_FTHPRC; 1.
KM	Receptor Transcription regulation: DNA binding: Nuclear protein:
EW	Transcript. Specif. 1. cis-acting. A trans-acting protein. Phosphorylation.
FT	DOMAIN 1 145 MODULATING.
FT	115 211 MODULATING RECEPTOR-TYPE.
FT	128 146 C4-TYPE.
FT	131 206 C4-TYPE.
FT	132 212 STEROID-BINDING.
FT	MOD_RES 84 PROSTIBORATION (BY SIMILARITY).
FT	485 485 PHOSTIBORATION (BY SIMILARITY).
FT	VASITAT 43 ME 557FE 55 ISOFORM BETA
FT	1).
SO	VASITAT 225 527 MISCTR(12) NR3A2-BETA (1).
SO	SEQUENCE 527 AA; 59120 MW; 9CD7A3BB9497EBA CR604;
Query Match	96.1%; Score 1157; DB 1; Length 527;
Post Local Similarity	94.8%; Prod. No. 5,26,98;

[14] J. H. Conway, *On numbers and games*, *Proc. London Math. Soc.* (3) **29** (1971), no. 1, 31–62.

insertion in the liquid binding domain as a putative dominant

[illegible]

-1- ALTERNATIVE PRODUCTS: AT LEAST 5 ISOPRENES: BETA-1 (SHOWN HERE),
 BETA-2, BETA-5, BETA-7A AND BETA-6; ARE PRODUCED BY ALTERNATIVE
 SPLICING.
 -1- TISSUE SPECIFICITY: EXPRESSED IN PROSTATE, OVARY, LEYDIG CELLS AND
 IN EPITHELIUM OF THE EPIDIDYMUS AND OF THE INITIAL SEGMEN
 OF THE EPIDIDYMUS.
 -1- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
 A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID BINDING DOMAIN.
 -1- SIMILARITY: BELONGS TO THE NOCLEAR HORMONE RECEPTORS FAMILY.
 NR4 SUBFAMILY.

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 OR SEND AN EMAIL TO LICENSE@isb.ch.

Query Match	93-44%	Score 110.8	EB 1	Length 530
Matches 215	Conservative	10	Mismatches 8	Indels 0
				Gaps 0
EMBL: U01451; AAC51132.1; -				
EMBL: AL000220; CAA03949.1; -				
EMBL: AF067432; AAC17919.1; ATL_INIT.				
EMBL: AF063858; AAC16656.1; -				
HSSP: P03372; HCP.				
GlycoSuiteDB: 008547; -				
MD: M01109492; EST2.				
InterPro: IPR000546; Hormone_rec_119.				
InterPro: IPR01223; Steroid_hormone_receptor.				
InterPro: IPR01628; Z1-C4.				
Plan: PF00104; Hormone_rec_1.				
Plan: P00105; Z1-C4; 1.				
PRINTS: PF00492; STEROHORMONF.				
PRINTS: PR00047; STEROIDINGER.				
SMART: SM00430; HOL1; 1.				
SMART: SM00399; ZNF_C4; 1.				
PROSITE: PS00631; NUCLEAR_RECEPTOR_1.				
Protein: Transcription regulation; DNA-binding; Nuclear protein; Zinc finger; Steroid binding; Alternative splicing; Glycoprotein; Phosphorylation.				
DOMAIN	1	148	MODULATING.	
DNA_BIND	149	214	NUCLEAR RECEPTOR-TYPE.	
ZN_FING	149	169	C4-TYPE.	
ZN_FING	185	209	C4-TYPE.	
FMAR	215	530	STEROID-BINDING.	
MOD_RES	61	61	PHOSPHORYLATION.	
MOD_RES	87	87	PHOSPHORYLATION (BY SIMILARITY).	
MOD_RES	105	105	PHOSPHORYLATION (BY MAPK) (PROBABLE).	
MOD_RES	488	488	PHOSPHORYLATION (BY SIMILARITY).	
CABINET	61	61	C-LINKED (GLYCAN).	
VARSPLOT	364	364	/PTID-GAN_000201.	
VARSPLOT	319	364	R -> RSSEDPHVAATKRSVPR (IN ISOFORM BETA-2).	
VARSPLOT	365	409	MISSING (IN ISOFORM BETA-5).	
VARSPLOT	319	409	MISSING (IN ISOFORM BETA-6).	
VARSPLOT	105	105	MISSING (IN ISOFORM BETA-5A).	
MUTAGEN	139	139	S->A: ABOLISHES STIMULATORY EFFECT OF RAS.	
MUTAGEN	139	139	S->A: NO LOSS OF THE STIMULATORY EFFECT OF RAS.	
CONFLICT	47	47	T -> A (IN REF. 2).	
CONFLICT	142	142	A -> T (IN REF. 2).	
CONFLICT	200	200	S -> N (IN REF. 2).	
CONFLICT	378	378	G -> D (IN REF. 2).	
CONFLICT	412	412	G -> H (IN REF. 2).	
CONFLICT	445	445	G -> P (IN REF. 2).	
CONFLICT	511	511	E -> G (IN REF. 2).	
SEQUENCE	530 AA.	59012 MW.	90573A161550ABF4 CR644;	

[illegible]

SEQUENCE FROM N.A.

ESTR4_MITCN

BA HAWKINS M.B., THORNTON J.W., CROWDS D., SKIPPER J.K., DODD A.,
THOMAS P.J.BA "Identification of a third distinct estrogen receptor and
its localization of estrogen receptors in teleosts."

BA Proc. Natl. Acad. Sci. U.S.A. 97:10751-10756(2000).

BA 1 FUNCTION: BINDS ESTROGEN WITH AN AFFINITY SIMILAR TO THAT OF
ER ALPHA, AND ACTIVATES EXPRESSION OF REPORTER GENES CONTAINING
ESTROGEN RESPONSE ELEMENTS (ERE) IN AN ESTROGEN-DEPENDENT MANNER.

BA 1 SUBUNIT: HOMO-DIMER (BY SIMILARITY).

BA 1 TISSUE SPECIFICITY: Abundant in the liver and testes, less
abundant in the ovary and barely detectable in the muscle.BA 1 LOCALIZATION: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
A DNA BINDING DOMAIN AND A C-TERMINAL STEROID BINDING DOMAIN.

BA 1 SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.

BA NCS SUBFAMILY.

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modified and this statement is not removed, usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/annouce/>
or send an email to license@isb-sib.ch).

BA EMBL: AF298192; AAC16712.1;

BA InterPro: IP0000546; Hormone_rec_119;

BA InterPro: IP000461; Steroid_intr;

BA InterPro: IP001723; Steroidhormone_recptor_1;

BA InterPro: IP001628; Z1_C4;

BA Pfam: PF00104; Hormone_rec_1;

BA Pfam: PF00105; Z1_C4_1;

BA PRINTS: PR00198; STROD0060NER;

BA PRINTS: PR00047; STROD0060NER;

BA SMART: SM00403; HOLL1.1;

BA SMART: SM00403; Z0E_C4_1;

BA TrEMBL: F00001; Steroid_hormone_1;

BA Description: Transcription regulation; DNA binding; Nuclear protein;

BA Zinc-finger; Steroid-binding;

BA ZINC-FINGER: 1; MODULATING;

BA DNA BIND: 182; 247; NUCLEAR RECEPTOR TYPE;

BA ZN_FING: 182; 202; C4 TYPE;

BA ZN_FING: 218; 242; C4 TYPE;

BA DOMAIN: 248; 653; STEROID BINDING;

BA SOURCE: 6/3 AA; 74680 MB; 280947577E001 CIR64;

Query Match 6/3 AA; Score 793; DB 1; Length 673;

Best Local Similarity: 67.7%; Pval: No. 5, 6e-66;

Matches: 154; Consistency: 47; Mismatches: 66; Indels: 2; Gaps: 2;

5. LLEAATGVV-LISRSATFTASMMMSITKIAKELVHMSWAKKIPGVPELSLPGVRL 63

424 LIDATGPEVLEMYKKPEFTASMMSTINIAKELVHMSWAKKIPGVPELSLPGVRL 483

64 LLSWVWVLEMLKWSGTHIEKELIAVLEDEKKEVGLIEHMLATSTIRRE 123

64 LLSWVWVLEMLKWSGTHIEKELIAVLEDEKKEVGLIEHMLATSTIRRE 111111

64 LK WLLILMLKWSGTHIEKELIAVLEDEKKEVGLIEHMLATSTIRRE 443

124 LKGVHLEMLKWSGTHIEKELIAVLEDEKKEVGLIEHMLATSTIRRE 182

111 LLSWVWVLEMLKWSGTHIEKELIAVLEDEKKEVGLIEHMLATSTIRRE 111111

444 LLSWVWVLEMLKWSGTHIEKELIAVLEDEKKEVGLIEHMLATSTIRRE 493

144 LLSWVWVLEMLKWSGTHIEKELIAVLEDEKKEVGLIEHMLATSTIRRE 221

104 LLSWVWVLEMLKWSGTHIEKELIAVLEDEKKEVGLIEHMLATSTIRRE 552

RESULT: 20

ESTR4_MITCN

BA HAWKINS M.B., THORNTON J.W., CROWDS D., SKIPPER J.K., DODD A.,
THOMAS P.J.BA "Identification of a third distinct estrogen receptor and
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BA InterPro: IP001723; Steroidhormone_recptor_1;

BA InterPro: IP001628; Z1_C4;

BA Pfam: PF00104; Hormone_rec_1;

BA Pfam: PF00105; Z1_C4_1;

BA PRINTS: PR00198; STROD0060NER;

BA PRINTS: PR00047; STROD0060NER;

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BA SMART: SM00403; Z0E_C4_1;

BA TrEMBL: F00001; Steroid_hormone_1;

BA Description: Transcription regulation; DNA binding; Nuclear protein;

BA Zinc-finger; Steroid-binding;

BA ZINC-FINGER: 1; MODULATING;

BA DNA BIND: 182; 247; NUCLEAR RECEPTOR TYPE;

BA ZN_FING: 182; 202; C4 TYPE;

BA ZN_FING: 218; 242; C4 TYPE;

BA DOMAIN: 248; 653; STEROID BINDING;

BA SOURCE: 6/3 AA; 74680 MB; 280947577E001 CIR64;

Query Match 6/3 AA; Score 793; DB 1; Length 673;

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5. LLEAATGVV-LISRSATFTASMMMSITKIAKELVHMSWAKKIPGVPELSLPGVRL 63

424 LIDATGPEVLEMYKKPEFTASMMSTINIAKELVHMSWAKKIPGVPELSLPGVRL 483

64 LLSWVWVLEMLKWSGTHIEKELIAVLEDEKKEVGLIEHMLATSTIRRE 123

64 LLSWVWVLEMLKWSGTHIEKELIAVLEDEKKEVGLIEHMLATSTIRRE 111111

64 LK WLLILMLKWSGTHIEKELIAVLEDEKKEVGLIEHMLATSTIRRE 443

124 LKGVHLEMLKWSGTHIEKELIAVLEDEKKEVGLIEHMLATSTIRRE 182

111 LLSWVWVLEMLKWSGTHIEKELIAVLEDEKKEVGLIEHMLATSTIRRE 111111

444 LLSWVWVLEMLKWSGTHIEKELIAVLEDEKKEVGLIEHMLATSTIRRE 493

144 LLSWVWVLEMLKWSGTHIEKELIAVLEDEKKEVGLIEHMLATSTIRRE 221

104 LLSWVWVLEMLKWSGTHIEKELIAVLEDEKKEVGLIEHMLATSTIRRE 552

1. X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 182-252.
 2. MENINGEAL-9402192; PubMed 8221995.
 3. Schwabe J.W.E., Chapman E., Finch J.T., Rhodes D.
 4. "The crystal structure of the estrogen receptor DNA-binding domain
 5. bound to DNA: how receptors discriminate between their response
 6. elements.";
 7. Cell 75:547-558(1993).
 8. 9. X-RAY CRYSTALLOGRAPHY (3.1 ANGSTROMS) OF 305-548.
 10. MENINGEAL-9478539; PubMed-9387390.
 11. PAPOZOWSKI J.A., Pike A.W., Taylor T., Hubbard R.E., Bern T.,
 12. "The structure of estrogen receptor-1: characterization of a
 13. molecular basis of agonism and antagonism in the estrogen
 14. receptor.";
 15. Nature 389:755-758(1997).
 16. 16. X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 306-544.
 17. MENINGEAL-96261297; PubMed-9609090.
 18. PAPOZOWSKI J.A., Ward V., Williams S.P., Slagter P.B.,
 19. "Crystallographic comparison of the estrogen and progesterone
 20. receptor's ligand binding domains.";
 21. Proc. Natl. Acad. Sci. U.S.A. 95:6336-6341(1998).
 22. 22. X-RAY CRYSTALLOGRAPHY (1.90 ANGSTROMS) OF 294-554.
 23. MENINGEAL-96091051; PubMed-9675647.
 24. ALLEN A.V., Wapner P., Loria P.M., Cheng L., Kushner P.J.,
 25. "The structural basis of estrogen receptor/coactivator recognition
 26. and the antagonism of this interaction by tamoxifen.";
 27. Cell 95:927-937(1998).
 28. 28. 29. 30. STRUCTURE MODELING OF 311-547.
 31. MENINGEAL-96280806; PubMed-9615007.
 32. MALLAT G.J., Xu W., Smith T., Mohr S.C.;
 33. "Molecular model for the ligand-binding domain of the human estrogen
 34. receptor.";
 35. J. Biomol. Struct. Dyn. 15:841-850(1998).
 36. 36. 37. VARIANT VAL-400.
 38. MENINGEAL-96280806; PubMed-9615007.
 39. Koda E., Millick A., Metzger D., Fongkittakornkul M., Park I.,
 40. Champion P.;
 41. "The cloned human estrogen receptor contains a mutation which alters
 42. its hormone binding properties.";
 43. EMBO J. 8:1981-1986(1989).
 44. 44. 45. VARIANT ALA-447.
 46. MENINGEAL-96280806; PubMed-9615007.
 47. Renese J.C., Katzenellenbogen R.S.;
 48. "Characterization of a temperature-sensitive mutation in the hormone
 49. binding domain of the human estrogen receptor. Studies in cell
 50. extracts and intact cells and their implications for
 51. hormone-dependent transcriptional activation.";
 52. J. Biol. Chem. 267:9868-9873(1992).
 53. 53. 54. VARIANT GLU-364.
 55. MENINGEAL-97126591; PubMed-8961252.
 56. Katzenellenbogen R.S., Ince B.A., Shapiro D.J., Katzenellenbogen R.S.;
 57. "A temperature-sensitive mutation in the estrogen receptor-1 of
 58. of dominant negative inhibitor of estrogen action.";
 59. Mol. Endocrinol. 10:1519-1526(1996).
 60. 60. 61. VARIANT CYS-160.
 62. MENINGEAL-97388672; PubMed-9196997.
 63. Wapner P., Loria P.M., Collins R., Warren M., Slagter P.,
 64. Estles R., Twitt R.M., Thompson S.P.D., Powsell M., Olsen A.O.,
 65. Mettler P., Stratton M.R., Beresford-Pale A.L.;
 66. "Screening for ESR mutations in breast and ovarian cancer patients.";
 67. Hum. Mutat. 9:541-549(1997).
 68. 68. 69. 70. 71. 72. 73. 74. 75. 76. 77. 78. 79. 80. 81. 82. 83. 84. 85. 86. 87. 88. 89. 90. 91. 92. 93. 94. 95. 96. 97. 98. 99. 100. 101. 102. 103. 104. 105. 106. 107. 108. 109. 110. 111. 112. 113. 114. 115. 116. 117. 118. 119. 120. 121. 122. 123. 124. 125. 126. 127. 128. 129. 130. 131. 132. 133. 134. 135. 136. 137. 138. 139. 140. 141. 142. 143. 144. 145. 146. 147. 148. 149. 150. 151. 152. 153. 154. 155. 156. 157. 158. 159. 160. 161. 162. 163. 164. 165. 166. 167. 168. 169. 170. 171. 172. 173. 174. 175. 176. 177. 178. 179. 180. 181. 182. 183. 184. 185. 186. 187. 188. 189. 190. 191. 192. 193. 194. 195. 196. 197. 198. 199. 200. 201. 202. 203. 204. 205. 206. 207. 208. 209. 210. 211. 212. 213. 214. 215. 216. 217. 218. 219. 220. 221. 222. 223. 224. 225. 226. 227. 228. 229. 230. 231. 232. 233. 234. 235. 236. 237. 238. 239. 240. 241. 242. 243. 244. 245. 246. 247. 248. 249. 250. 251. 252. 253. 254. 255. 256. 257. 258. 259. 260. 261. 262. 263. 264. 265. 266. 267. 268. 269. 270. 271. 272. 273. 274. 275. 276. 277. 278. 279. 280. 281. 282. 283. 284. 285. 286. 287. 288. 289. 290. 291. 292. 293. 294. 295. 296. 297. 298. 299. 300. 301. 302. 303. 304. 305. 306. 307. 308. 309. 310. 311. 312. 313. 314. 315. 316. 317. 318. 319. 320. 321. 322. 323. 324. 325. 326. 327. 328. 329. 330. 331. 332. 333. 334. 335. 336. 337. 338. 339. 340. 341. 342. 343. 344. 345. 346. 347. 348. 349. 350. 351. 352. 353. 354. 355. 356. 357. 358. 359. 360. 361. 362. 363. 364. 365. 366. 367. 368. 369. 370. 371. 372. 373. 374. 375. 376. 377. 378. 379. 380. 381. 382. 383. 384. 385. 386. 387. 388. 389. 390. 391. 392. 393. 394. 395. 396. 397. 398. 399. 400. 401. 402. 403. 404. 405. 406. 407. 408. 409. 410. 411. 412. 413. 414. 415. 416. 417. 418. 419. 420. 421. 422. 423. 424. 425. 426. 427. 428. 429. 430. 431. 432. 433. 434. 435. 436. 437. 438. 439. 440. 441. 442. 443. 444. 445. 446. 447. 448. 449. 450. 451. 452. 453. 454. 455. 456. 457. 458. 459. 460. 461. 462. 463. 464. 465. 466. 467. 468. 469. 470. 471. 472. 473. 474. 475. 476. 477. 478. 479. 480. 481. 482. 483. 484. 485. 486. 487. 488. 489. 490. 491. 492. 493. 494. 495. 496. 497. 498. 499. 500. 501. 502. 503. 504. 505. 506. 507. 508. 509. 510. 511. 512. 513. 514. 515. 516. 517. 518. 519. 520. 521. 522. 523. 524. 525. 526. 527. 528. 529. 530. 531. 532. 533. 534. 535. 536. 537. 538. 539. 540. 541. 542. 543. 544. 545. 546. 547. 548. 549. 550. 551. 552. 553. 554. 555. 556. 557. 558. 559. 560. 561. 562. 563. 564. 565. 566. 567. 568. 569. 570. 571. 572. 573. 574. 575. 576. 577. 578. 57

[illegible]

[illegible]

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      68.1%; Score 745.5; Jm 1; Length 525;
      Best Local Similarity 63.9%; Prod No R 50-62;
      Matches 146; Conservative 45; Indels 3; Caps 2;
02 2 VILLAEPRVLSNR SATPEASNNMSTRALKEVHMLSWAKTTEVILSTP 59
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| D10 | 274 | QVELLESWEEVMELTWRSIRPKLIFADILLDRSEHSVENMAETHTMLATISK | 448 |
| D11 | | | |
| D12 | 129 | EPELEPHGHLSVAMMLLSMVAALAAALASDRAAASGVATAVAVAYAN | 178 |
| D13 | | | |
| D14 | 179 | LSSSGEMFADMLLREVFHASNSDEHLIRPTFRVVVYVYLTPRDNAEYAI | 241 |
| D15 | | | |
| D16 | 584 | CSAWGGSPGADLLLSHPISMNSMBHLYSMDCKNVHVDLLLMEDAH | 448 |
| D17 | | | |
| D18 | RESULT_29 | | |
| D19 | ESRL_CENTRI | | |
| D20 | TRF_CENTRI | STRANDS: | PRT: 585 AA. |
| D21 | QVYH43 | | |
| D22 | 16-OCT-2001 (rel. 40; Created) | | |
| D23 | 16-OCT-2001 (rel. 40; Last sequence update) | | |
| D24 | 16-OCT-2001 (rel. 40; Last annotation update) | | |
| D25 | Estrogen receptor (ER) (estradiol receptor) (ER-alpha) | | |
| D26 | ESTR_OB_NBAI_OB_PSR | | |
| D27 | Oreochromis niloticus (Nile tilapia) (tilapia nilotica); | | |
| D28 | Eicharya, Melur, Chajaca, Gaudin, Vertebatae; Euteleostomi; | | |
| D29 | Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoactopteri; | | |
| D30 | Acanthomorpha; Acanthopterygii; Percomorphia; Perciformes; Labroidae; | | |
| D31 | Cichlidae; Oreochromis. | | |
| D32 | MOL_TAXID=8128; | | |
| D33 | [1] | | |
| D34 | SEQUENCE FROM N.A. | | |
| D35 | Chang X.T., Katsuyoshi T., Tojo T., Yoshitara Y., Ikemuchi T., | | |
| D36 | Kajihira H., Nakamura M., Nagahama Y.; | | |
| D37 | "cDNA sequence of Tilapia type alpha estrogen receptor."; | | |
| D38 | Submitted (oct-1999) to the FBL/GenBank/EBI databases. | | |
| D39 | -1- FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN | | |
| D40 | THE REGULATION OF ENDOCRINE GENE EXPRESSION AND APPLIC CELLULAR | | |
| D41 | PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES. | | |
| D42 | 1- ECDFUNT: BINDS DNA AS A HOMODIMER, CAN FORM A HETERODIMER WITH PR- | | |
| D43 | OCTA (BY SIMILARITY). | | |
| D44 | -1- SUBCELLULAR LOCATION: Nucleol. | | |
| D45 | -1- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN, | | |
| D46 | A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN. | | |
| D47 | -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY. | | |
| D48 | NK3 SUBFAMILY. | | |
| D49 | | | |
| D50 | | | |
| D51 | This SWISS-Prot entry is copyright. It is produced through a collaboration | | |
| D52 | between the Swiss Institute of Bioinformatics and the FBL/annotation - | | |
| D53 | the European Bioinformatics Institute. There are no restrictions on its | | |
| D54 | use by non profit institutions as long as its content is in no way | | |
| D55 | modified and this statement is not removed, usage by and for commercial | | |
| D56 | or send an email to license@sbcb.ch) | | |
| D57 | | | |
| D58 | FBIHL_02EG34; ZAD00245.1; * | | |
| D59 | HSSP: P03372; IBCP. | | |
| D60 | InterPro: IPR000546; Hormone_rec_Lin. | | |
| D61 | InterPro: IPR001292; oest_recep. | | |
| D62 | InterPro: IPR001729; Steroid_hormone_receptor. | | |
| D63 | InterPro: IPR001628; st_o4. | | |
| D64 | pFam: PF00104; hormone_rec_1 | | |
| D65 | pFam: PF02159; oest_recept_1 | | |
| D66 | pFam: PF00105; st_o4_1 | | |
| D67 | pFam: PF00398; steroid_horm_r | | |
| D68 | pFam: PF00047; steroid_inchr. | | |
| D69 | SMART: SM00430; HOLL_1 | | |
| D70 | SMART: SM00399; zst_o4_1 | | |
| D71 | PROSITE: PS00031; NUTR_FAM_RECEPTOR_1 | | |
| D72 | Receptor: Transcription regulation; DNA-binding; Nuclear proteins | | |
| D73 | Zinc-finger; Steroid-binding. | | |
| D74 | zinc-famr_1 | 138 | MOTIF: (BY SIMILARITY). |
| D75 | DNA_BIND | 139 | 204 |
| D76 | | | NUCLEAR RECEPTOR-TYPE. |

GenBank version 4.5
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M protein - protein search, using sw model

July 12, 2002, 14:41:15 : Search time: 46.45 seconds

(without alignments)
867,768 Million cell updates/sec

Database: 08-08-826-361a-4

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Search: 1 EMBL/AF016774/USP5A.....CANVYVYVLLHMLNHL 233

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 112.5 | 94.2 | 526 | 6 | 09B0W5 |
| 2 | 108.4 | 91.8 | 504 | 11 | 091286 |
| 3 | 101.2 | 85.7 | 459 | 6 | 095ME0 |
| 4 | 95.8 | 80.7 | 486 | 6 | 095ME9 |
| 5 | 90.5 | 76.3 | 542 | 13 | 090766 |
| 6 | 84.1 | 71.2 | 592 | 13 | 090MS9 |
| 7 | 83.8 | 71.0 | 591 | 13 | 098SM8 |
| 8 | 82.6 | 67.9 | 553 | 13 | 090MS8 |
| 9 | 81.8 | 69.3 | 553 | 13 | 098SM7 |
| 10 | 74.2 | 62.8 | 431 | 6 | 095113 |
| 11 | 70.8 | 59.9 | 569 | 13 | 098SM9 |
| 12 | 70.2 | 59.4 | 620 | 13 | 090WH6 |
| 13 | 70.1 | 59.4 | 564 | 13 | 090WV1 |
| 14 | 69.5 | 59.0 | 458 | 13 | 090J33 |
| 15 | 66.2 | 56.1 | 554 | 13 | 090ZM8 |
| 16 | 60.9 | 51.4 | 276 | 13 | 091984 |

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| 17 | 590.5 | 50.0 | 445 | 13 | 090B24 | 090B24 microtubule |
| 18 | 517.5 | 43.8 | 159 | 6 | 046492 | 046492 sus scrofa |
| 19 | 487 | 41.2 | 250 | 6 | 095100 | 095100 canis familiaris |
| 20 | 451.5 | 38.2 | 208 | 13 | 090259 | 090259 brachydanio |
| 21 | 442 | 37.4 | 87 | 6 | 090B92 | 090B92 sus scrofa |
| 22 | 421.5 | 35.9 | 344 | 4 | 0902M1 | 0902M1 homo sapiens |
| 23 | 351.5 | 29.9 | 125 | 6 | 019009 | 019009 equus caballus |
| 24 | 325 | 27.5 | 323 | 4 | 096182 | 096182 homo sapiens |
| 25 | 291.5 | 24.7 | 106 | 13 | 090X52 | 090X52 sus scrofa |
| 26 | 269.5 | 22.8 | 237 | 4 | 090B84 | 090B84 homo sapiens |
| 27 | 251.5 | 21.3 | 484 | 5 | 090SE9 | 090SE9 drosophila |
| 28 | 238 | 20.2 | 583 | 13 | 090E94 | 090E94 xenopus laevis |
| 29 | 236 | 20.0 | 732 | 13 | 090B09 | 090B09 xenopus laevis |
| 30 | 231.5 | 19.6 | 939 | 6 | 090J00 | 090J00 canis familiaris |
| 31 | 231 | 19.6 | 298 | 6 | 028547 | 028547 canis familiaris |
| 32 | 227 | 19.2 | 438 | 13 | 090B87 | 090B87 canis familiaris |
| 33 | 226.5 | 19.2 | 284 | 13 | 090B00 | 090B00 porphyrio |
| 34 | 224 | 19.0 | 438 | 13 | 090418 | 090418 brachydanio |
| 35 | 224 | 19.0 | 692 | 13 | 090B74 | 090B74 brachydanio |
| 36 | 224.5 | 18.9 | 363 | 5 | 090AP1 | 090AP1 brachydanio |
| 37 | 222 | 18.8 | 196 | 6 | 018993 | 018993 canis familiaris |
| 38 | 222 | 18.8 | 366 | 13 | 042274 | 042274 streptococcus |
| 39 | 222 | 18.8 | 525 | 6 | 095153 | 095153 mus musculus |
| 40 | 222 | 18.8 | 710 | 13 | 091B05 | 091B05 drosophila |
| 41 | 219 | 18.5 | 412 | 13 | 091B40 | 091B40 xenopus laevis |
| 42 | 218 | 18.5 | 448 | 13 | 091425 | 091425 canis familiaris |
| 43 | 216 | 18.3 | 231 | 4 | 096410 | 096410 homo sapiens |
| 44 | 216 | 18.3 | 400 | 5 | 061448 | 061448 andersonia |
| 45 | 215 | 18.2 | 427 | 5 | 090C48 | 090C48 apus moctill |

ALIGNMENTS

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AC 09B0W5:
DT 01-JUN-2001 (TEMBL:01, 17, created)
DI 01-JUN-2001 (TEMBL:01, 17, last sequence update)
DT 01-JUN-2001 (TEMBL:01, 17, last sequence update)
DE ESTROGEN RECEPTOR BETA.
GN ER BETA.
OS Sus scrofa (pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI:taxid:9623;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE: OVARY;
FA LAYOIE H.A.; Lesimine D.A.;
RT "Cloning and expression of estrogen receptor beta isoforms from porcine ovary."
RT PubMed:10300000.
RL Funder:Biochemistry 1999;39(20):3700-3705.
CC -!- SIMILARITY: RELATIONS: NUCLEAR (BY SIMILARITY).
CC -!- SIMILARITY: RELATIONS: TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
CC EMBL: AF267746; AAK15151.1; -;
DR EMBL: P03372; 1H9V.
DR HSSP: P03372; 1H9V.
DR InterPro: IPR000546; Hormone_rec_1b.
DR InterPro: IPR001723; Steroidhormone_receptor.
DR InterPro: IPR001628; Z1-c4.
DR Pfam: PF00105; Hormone_rec_1.
DR Pfam: PF00105; Z1-c4; 1.
DR PRINTS: PR00498; STRIDHOMNER.
DR PRINTS: PR00497; STRIDHOMNER.
DR SMART: SM00430; HELL; 1.
DR SMART: SM00399; ZNF_C4; 1.
DR PROSITE: PS00031; NUCLEAR_RECEPTOR; 1.
DR DNA-binding: Nuclear protein; Receptor; Transcription regulation;
KW Zinc-finger.
SU SEQUENCE 526 AA; 58847 MW; 346D847621F814C CRC64;

[illegible]

GenCore version 4.5
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[illegible]

| Year | Search time (seconds) | Without alignments |
|--------------|-----------------------|----------------------------------|
| 2017-12-2002 | 14,457,477 | 161,433 Million cell updates/sec |

1. "AVSTROYANSKIY VINITAT, ... ENERGIYA" BLKRETIYOM 66

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total number of hits satisfying chosen parameters: 105224

Maximum for Seq Length: 0
Maximum for Seq Length: 2000000000

Maximum Match Took
List for first 45 summaries
$$f_0 = \frac{1}{\pi} \int_{-\infty}^{\infty} f(x) dx$$

Proof. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SIMMAKITS

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| 2 | 486 | 100.0 | 472 | 1 | ESR2_XINIA |
| 3 | 386 | 100.0 | 526 | 1 | ESR2_PIG |
| 4 | 386 | 100.0 | 527 | 1 | ESR2_PIGV |
| 5 | 386 | 100.0 | 527 | 1 | ESR2_SHEEP |
| 6 | 386 | 100.0 | 520 | 1 | ESR2_CALIA |
| 7 | 386 | 100.0 | 540 | 1 | ESR2_HUMAN |
| 8 | 386 | 100.0 | 540 | 1 | ESR2_MOUSE |
| 9 | 386 | 100.0 | 554 | 1 | ESR2_STUVE |
| 10 | 386 | 100.0 | 568 | 1 | ESR1_CABAU |
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| 15 | 386 | 100.0 | 569 | 1 | ESR1_MHARE |
| 16 | 381 | 98.7 | 530 | 1 | ESR1_RAT |
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| 97 | 386 | 98.4 | 561 | 1 | ESR1_PADMA |
| 98 | 386 | 98.4 | 561 | 1 | ESR1_PADMA |
| 99 | 386 | 98.4 | 561 | 1 | ESR1_PADMA |
| 100 | 386 | 98.4 | 561 | 1 | ESR1_PADMA |

[illegible]

1 FUNCTION: BINDS ESTROGEN WITH AN AFFINITY SIMILAR TO THAT OF
2 ER ALPHA AND ACTIVATES EXPRESSION OF REPORTER GENES CONTAINING
3 ESTROGEN RESPONSE ELEMENTS (ERE) IN AN ESTROGEN DEPENDENT MANNER.
4 SUBUNIT: BINDS ERA AS A DIMER; CAN FORM A DIMEROMER WITH ER
5 ALPHA (BY SIMILARITY).
6 SUBCELLULAR LOCATION: NUCLEUS.
7 DOMAIN: COMPOSED OF THREE DOMAINS: A REGULATING N-TERMINAL DOMAIN,
8 A DNA BINDING DOMAIN AND A C-TERMINAL STEROID BINDING DOMAIN.
9 SIMILARITY: BELONGS TO THE REGULAR HORMONE RECEPTORS FAMILY.
10 NR3 SUBFAMILY.

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13 the European Bioinformatics Institute. There are no restrictions on its
14 use by non-profit institutions as long as its content is in no way
15 modified and this statement is not removed. Usage by and for commercial
16 entities requires a license agreement (see <http://www.isb-sib.ch/announcements>
17 or send an email to license@isb.sib.ch).

18 EMBL: A604269; AAB26924.1;
19 HESR: J03472; IEDT;
20 InterPro: IPR000536; Hormone_rec_11q;
21 InterPro: IPR016281; Z1_C4;
22 Pfam: PF00104; Hormone_rec_1;
23 Pfam: PF00105; Z1_C4; 1;
24 PRINTS: PK00498; STROBOMER;
25 PRINTS: PK00472; STROBPINGER;
26 SMART: SM00403; BOLL; 1;
27 SMART: SM00399; ZNF_C4; 1;
28 PROSITE: PS00041; NUCLEAR RECEPTOR; 1;
29 Receptor; Transcription regulation; DNA binding; Nuclear protein;
30 Zinc finger; Steroid binding.
31 Domain
32 F1 INA_RING 178 243 NUCLEAR RECEPTOR TYPE;
33 F1 ZN_RING 178 198 C4 TYPE;
34 F1 ZN_RING 206 240 C4 TYPE;
35 F1 DOMAIN 244 568 STEROID-BINDING;
36 SDOUSRY: 568 AA; 6.45 kD MW; 20878077500649 GRCv44;

Query Match 100.0%; Score 386; DB 1; Length 568;
Best Local Similarity 100.0%; Pred. No. 2,40-45;
Matches 66; Conserved 0; Mismatches 0; Gaps 0;
UY 61 CYEVM 66
111111
DB 248 CYEVM 244

RESULT 11
ID ESR2_ORF6 STANDARD; PRI: 568 AA;
AC P57292;
DT 01-OCT-2001 (Ref. 40; Created)
DT 01-OCT-2001 (Ref. 40; Last sequence update)
DT 16-OCT-2001 (Ref. 40; Last annotation update)
DE Estrogen receptor beta (ER beta).
GN ESR2 OR NR3A2;
OS Homo sapiens (Homo sapiens) (Mammalia: Euteleostomi;
Chordata: Vertebrata: Euteleostomi;
Actinopterygii: Neopterygii: Teleostei: Euteleostei;
Perciformes: Labroidae;
Nili: Labridae).
RN 111
RS SEQUENCE FROM N.A.
RA Bouvier M., Akrakian G., Fret K.;
RT "Molecular cloning of an estrogen receptor beta subtype from rainbow
fish (*Oryzias latipes*)."
RT Submitted (01-2000) to the EMBL/GenBank/Trna databases;
RT 1. FUNCTION: BINDS ESTROGEN WITH AN AFFINITY SIMILAR TO THAT OF

1 ER ALPHA AND ACTIVATES EXPRESSION OF REPORTER GENES CONTAINING
2 ESTROGEN RESPONSE ELEMENTS (ERE) IN AN ESTROGEN DEPENDENT MANNER.
3 SUBUNIT: BINDS ERA AS A DIMER; CAN FORM A DIMEROMER WITH ER
4 ALPHA (BY SIMILARITY).
5 SUBCELLULAR LOCATION: NUCLEUS.
6 DOMAIN: COMPOSED OF THREE DOMAINS: A REGULATING N-TERMINAL DOMAIN,
7 A DNA BINDING DOMAIN AND A C-TERMINAL STEROID BINDING DOMAIN.
8 SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
9 NR3 SUBFAMILY.

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15 entities requires a license agreement (see <http://www.isb-sib.ch/announcements>
16 or send an email to license@isb.sib.ch).

17 EMBL: A1269883; CA20714.1;
18 InterPro: IPR001233; Steroidhormone_receptor;
19 InterPro: IPR016281; Z1_C4;
20 Pfam: PF00104; Hormone_rec_1;
21 Pfam: PF00105; Z1_C4; 1;
22 PRINTS: PK00498; STROBOMER;
23 PRINTS: PK00472; STROBPINGER;
24 SMART: SM00403; BOLL; 1;
25 SMART: SM00399; ZNF_C4; 1;
26 PROSITE: PS00041; NUCLEAR RECEPTOR; 1;
27 Receptor; Transcription regulation; DNA binding; Nuclear protein;
28 Zinc finger; Steroid binding.
29 Domain
30 F1 INA_RING 178 243 NUCLEAR RECEPTOR TYPE;
31 F1 ZN_RING 178 198 C4 TYPE;
32 F1 ZN_RING 214 248 C4 TYPE;
33 F1 DOMAIN 244 568 STEROID-BINDING;
34 SDOUSRY: 568 AA; 6.813 kD MW; P7A70781822804 GRCv44;

Query Match 100.0%; Score 386; DB 1; Length 568;
Best Local Similarity 100.0%; Pred. No. 2,40-45;
Matches 66; Conserved 0; Mismatches 0; Gaps 0;
UY 61 CYEVM 66
111111
DB 248 CYEVM 244

RESULT 12
ID ESR1_ORF6 STANDARD; PRI: 584 AA;
AC P50240;
DT 01-OCT-1996 (Ref. 34; Created)
DT 01-NOV-1997 (Ref. 35; Last sequence update)
DT 16-OCT-2001 (Ref. 40; Last annotation update)
DE Estrogen receptor (ER) (Estrogen receptor) (ER-alpha).
GN ESR1 OR NR3A1 OR ESR;
OS Homo sapiens (Homo sapiens) (Mammalia: Euteleostomi;
Chordata: Vertebrata: Euteleostomi;
Actinopterygii: Neopterygii: Teleostei: Euteleostei;
Perciformes: Labroidae;
Nili: Labridae).
RN 111
RS SEQUENCE FROM N.A.
RA Bouvier M., Akrakian G., Fret K.;
RT "Molecular cloning of an estrogen receptor beta subtype from rainbow
fish (*Oryzias latipes*)."
RT Submitted (01-2000) to the EMBL/GenBank/Trna databases;
RT 1. FUNCTION: BINDS ESTROGEN WITH AN AFFINITY SIMILAR TO THAT OF


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CC use by non profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
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CC or send an email to license@ebi.ac.uk).
CC
DR PMID: A1060639; CADG1479.1; -
DR EMBL: AF136979; AAD31042.1; -
DR EMBL: AF013104; AAB84248.1; -
DR ISSP: P03372; HGPC.
DR InterPro: IPR000536; Hormone_rec_1fq.
DR InterPro: IPR001723; Steroidhormone_receptor.
DR InterPro: IPR001628; zt-C4.
DR Pfam: PF00104; hormone_rec_1.
DR Pfam: PF00105; zt-C4_1.
DR PRINTS: PS00399; STEROID-REPR.
DR PRINTS: PR00047; STROIDFINGER.
DR SMART: SM00430; HOL1_1.
DR SMART: SM00399; ZNF_C4_1.
DR PROSITE: PS00031; NUCLEAR_RECEPTOR; 1.
KW Receptor; Transcription regulation; DNA-binding; Nuclear protein;
KW Zinc-finger; Steroid-binding
FT DOMAIN 1 142 REGULATING (BY SIMILARITY).
FT ZN_FING 143 168 NUCLEAR RECEPTOR-TYPE.
FT ZN_FING 179 203 CA-TYPE.
FT ZN_FING 179 203 C4-TYPE.
FT DOMAIN 209 270 HISTONE.
FT DOMAIN 271 579 STEROID-BINDING (BY SIMILARITY).
FT DOMAIN 259 263 POLY-GLY.
FT DOMAIN 533 537 POLY-SER.
FT CONFLICT 83 86 QPAN -> HPET (IN REF. 2).
FT CONFLICT 98 98 Y > YES (IN REF. 2).
FT CONFLICT 480 480 K > N (IN REF. 3).
SQ SOURCE 579 AA: 63361 MW: 76116ZARC56371F CRC64:
Query Match 98.4%; Score 380; DB 1; Length 579;
Best Local Similarity 97.0%; pred. No. 1,16-34;
Matches 64; Conservative 2; Mismatch 0; Indels 0; Gaps 0;
2 1 CAV-STYAS-VNHVWQGVCTEATKFSLEGNYVTAIN-QT-GRHFFSA-N-60
2b 143 CAVSGAGACVMHWAS-DCA-KAIFRSIQHRETMELAIWCCTLRERDS-CAV-RNR-292
QY 61 CYEGVM 66
DB 203 CYECVM 208
RESULT 20
ESRI_PAGMA STANDARD; PRI: 581 AA.
ID ESRI_PAGMA STANDARD; PRI: 581 AA.
GC 042132;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Estrogen receptor (ER) (Estradiol receptor) (R-alpha).
GN ESRI [NP 581] NP ER.
OS Pirus major (ped sea bream) (Phrygerythrus major).
OC Actinopterygii; Neofurculi; Teleostei; Fidelestei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Percoidae;
OC Sparidae; Pagrus.
OX NCBI_taxid=143350;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
FA Tachia K., Kinoshita M., Tojohara H., Sakaguchi M.;
RT "Sequence and expression of a cDNA encoding the red seabream estrogen
RT receptor";
RI Fishbases Sci-1 64-141-135(1999)

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1 PREDICTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN
 2 THE REGULATION OF ENHANCING OF GENE EXPRESSION AND AFFECT CELLULAR
 3 PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.
 4 SUBUNIT BINDS DNA AS A HOMODIMER. CAN FORM A HETERODIMER WITH ER-
 5 ALPHA (BY SIMILARITY).
 6 SUBCELLULAR LOCATION: Nucleus.
 7 DOMAIN: COMPOSED OF THREE DOMAINS: A REGULATING N-TERMINAL DOMAIN,
 8 A DNA BINDING DOMAIN AND A C-TERMINAL STEROID BINDING DOMAIN.
 9 SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
 10 NO SUBFAMILY.
 11
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 17 entities requires a license agreement (See <http://www.ebi.ac.uk/seqdb/doc/0.9.0/>
 18 or send an email to license@ebi.ac.uk).
 19
 20 EMBL: A0001453; BAA25617.1;
 21 ECRD: P04472; HRPD;
 22 InterPro: IP0000546; Hormone_rec_119;
 23 InterPro: IP0001292; oest_recep;
 24 InterPro: IP0001243; Steroidhormone_receptor;
 25 InterPro: IP0001628; Z1_C4;
 26 Pfam: PF00159; hormone_rec_1;
 27 Pfam: PF02159; oest_recep_1;
 28 Pfam: PF00159; Z1_C4_1;
 29 PRINTS: PR00198; STEROIDHORMONE-REC;
 30 PRINTS: PR00047; STEROIDRECEPTER;
 31 SMART: SM00403; HOL1_1;
 32 SMART: SM00403; HOL1_1;
 33 ProSITE: PS00041; NUCLEAR RECEPTOR 1;
 34 ProSITE: PS00041; NUCLEAR RECEPTOR 1;
 35 ProSITE: PS00041; NUCLEAR RECEPTOR 1;
 36 ProSITE: PS00041; NUCLEAR RECEPTOR 1;
 37 ProSITE: PS00041; NUCLEAR RECEPTOR 1;
 38 ProSITE: PS00041; NUCLEAR RECEPTOR 1;
 39 ProSITE: PS00041; NUCLEAR RECEPTOR 1;
 40 ProSITE: PS00041; NUCLEAR RECEPTOR 1;
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 97 ProSITE: PS00041; NUCLEAR RECEPTOR 1;
 98 ProSITE: PS00041; NUCLEAR RECEPTOR 1;
 99 ProSITE: PS00041; NUCLEAR RECEPTOR 1;
 100 ProSITE: PS00041; NUCLEAR RECEPTOR 1;

1 ESTIMATED: Hypothetical.
 2 NCBJ: J0410 57229;
 3 [1]
 4 SEQUENCE FROM N. A.
 5 TISSUE Hypothetical;
 6 MEDLINE 97163508; PubMed 9010328;
 7 Jacobs E.C.; Arnold A.P.; Campanoni A.T.;
 8 "Zebra Finch estradiol receptor cDNA: cloning and mRNA expression.";
 9 J. Steroid Biochem. Mol. Biol. 59:145, 145(1996).
 10 PREDICTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN
 11 THE REGULATION OF GENE EXPRESSION AND AFFECT CELLULAR
 12 PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.
 13 SUBUNIT BINDS DNA AS A HOMODIMER. CAN FORM A HETERODIMER WITH ER
 14 ALPHA (BY SIMILARITY).
 15 SUBCELLULAR LOCATION: Nucleus.
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 27 or send an email to license@ebi.ac.uk).
 28
 29 EMBL: L79911; A0001108.1;
 30 ECRD: P04472; HRPD;
 31 InterPro: IP0000546; Hormone_rec_119;
 32 InterPro: IP0001292; oest_recep;
 33 InterPro: IP0001243; Steroidhormone_receptor;
 34 InterPro: IP0001628; Z1_C4;
 35 Pfam: PF00159; hormone_rec_1;
 36 Pfam: PF02159; oest_recep_1;
 37 Pfam: PF00159; Z1_C4_1;
 38 PRINTS: PR00198; STEROIDHORMONE-REC;
 39 PRINTS: PR00047; STEROIDRECEPTER;
 40 SMART: SM00403; HOL1_1;
 41 SMART: SM00403; HOL1_1;
 42 ProSITE: PS00041; NUCLEAR RECEPTOR 1;
 43 ProSITE: PS00041; NUCLEAR RECEPTOR 1;
 44 ProSITE: PS00041; NUCLEAR RECEPTOR 1;
 45 ProSITE: PS00041; NUCLEAR RECEPTOR 1;
 46 ProSITE: PS00041; NUCLEAR RECEPTOR 1;
 47 ProSITE: PS00041; NUCLEAR RECEPTOR 1;
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 97 ProSITE: PS00041; NUCLEAR RECEPTOR 1;
 98 ProSITE: PS00041; NUCLEAR RECEPTOR 1;
 99 ProSITE: PS00041; NUCLEAR RECEPTOR 1;
 100 ProSITE: PS00041; NUCLEAR RECEPTOR 1;

[illegible]

Mon Jul 15 08:11:03 2002

us-08-826-361a-3.rsp

Page 22

•
•
•

CC DNA encoding estrogen receptor - useful in screening assay to
 CC identify novel ligands or hormonal analogues

XX Claim 4: Page 45-47; 45pp; English.

CC This sequence represents a novel estrogen binding protein isolated from
 CC human testis cDNA in order to study upstream transcription initiation
 CC codons using 5' RACE-PCR technology. This receptor is able to bind and
 CC be activated by estradiol, estrone and estrilol, can be used in a screening
 CC assay for the identification of new drugs e.g. novel ligands or hormonal
 CC analogues.

XX Sequence: 540 AA:

Query Match: 100.0%; Score 1181; DB ID: Length 540;
 Host Local Similarity: 100.0%; Prod. No. 4, 36-1227

Matches: 2343; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

1 LVLLLEAPPPHVLISPPSAFTFASMMMSSTRIAPNVLVMMISWAKIPGVSTFPG 60
 269 LVLLLEAPPPHVLISPPSAFTFASMMMSSTRIAPNVLVMMISWAKIPGVSTFPG 120
 428 LVLLLEAPPPHVLISPPSAFTFASMMMSSTRIAPNVLVMMISWAKIPGVSTFPG 180
 587 LVLLLEAPPPHVLISPPSAFTFASMMMSSTRIAPNVLVMMISWAKIPGVSTFPG 240
 746 LVLLLEAPPPHVLISPPSAFTFASMMMSSTRIAPNVLVMMISWAKIPGVSTFPG 300
 905 LVLLLEAPPPHVLISPPSAFTFASMMMSSTRIAPNVLVMMISWAKIPGVSTFPG 360
 1064 LVLLLEAPPPHVLISPPSAFTFASMMMSSTRIAPNVLVMMISWAKIPGVSTFPG 420
 1223 LVLLLEAPPPHVLISPPSAFTFASMMMSSTRIAPNVLVMMISWAKIPGVSTFPG 480
 1382 LVLLLEAPPPHVLISPPSAFTFASMMMSSTRIAPNVLVMMISWAKIPGVSTFPG 540

RESULT 4

AAW7858: AAW7858 standard; Protein: 540 AA.

XX AAW7858: AAW7858 standard; Protein: 540 AA.

XX 07-JUN-1999 (first entry)

XX Human estrogen receptor-beta.

XX Estrogen receptor beta; ER-beta; human.

XX Homo sapiens.

XX W0907847 AL.

XX 16-DEC-1999.

XX 20-SEP-2001: 9860-0814944.

XX 15-MAR-2001: 9705-0906465.

XX (AMMP-3) AMERICAN HOME Product Group

XX Blat RA, Henderson RA, Hsiao C, Karathanasis SK;

XX WPI: 1999-167424/14.

XX N-ESTR: AAX464.

XX Human estrogen receptor-beta coding sequence - useful in the

XX production of human estrogen receptor-beta and identification of

XX human estrogen receptor-beta interactive compounds

XX Claim 17: Page 42-44; 49pp; English.

XX This polypeptide comprises a full-length human estrogen receptor-beta

XX (ER-beta), including 45 previously unknown N-terminal amino acids

CC residues that are believed to contribute to the transcription

CC activation function of the receptor. The amino acid sequence was

CC deduced from the nucleotide sequence (see AAX2464) of an isolated

CC cDNA clone. ER-beta is selectively expressed in the thymus,

CC spleen, ovary and testes. The invention encompasses ER-beta

CC polypeptides and polypeptides, particularly peptides which

CC include residues 1-15 of ER-beta. The invention also provides

CC expression systems in which transcriptionally active ER-beta or

CC ER-beta can be produced, as well as screening methods for

CC identifying ER-beta agonists and antagonists (including

CC tissue-specific agonists and anti-estrogens), and ER-beta

CC co-activators and inhibitors.

XX Sequence: 540 AA:

Query Match: 100.0%; Score 1181; DB ID: Length 540;
 Host Local Similarity: 100.0%; Prod. No. 4, 36-1227

Matches: 2343; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

1 LVLLLEAPPPHVLISPPSAFTFASMMMSSTRIAPNVLVMMISWAKIPGVSTFPG 60
 269 LVLLLEAPPPHVLISPPSAFTFASMMMSSTRIAPNVLVMMISWAKIPGVSTFPG 120
 428 LVLLLEAPPPHVLISPPSAFTFASMMMSSTRIAPNVLVMMISWAKIPGVSTFPG 180
 587 LVLLLEAPPPHVLISPPSAFTFASMMMSSTRIAPNVLVMMISWAKIPGVSTFPG 240
 746 LVLLLEAPPPHVLISPPSAFTFASMMMSSTRIAPNVLVMMISWAKIPGVSTFPG 300
 905 LVLLLEAPPPHVLISPPSAFTFASMMMSSTRIAPNVLVMMISWAKIPGVSTFPG 360
 1064 LVLLLEAPPPHVLISPPSAFTFASMMMSSTRIAPNVLVMMISWAKIPGVSTFPG 420
 1223 LVLLLEAPPPHVLISPPSAFTFASMMMSSTRIAPNVLVMMISWAKIPGVSTFPG 480
 1382 LVLLLEAPPPHVLISPPSAFTFASMMMSSTRIAPNVLVMMISWAKIPGVSTFPG 540

RESULT 5

AAE10457: AAE10457 standard; Protein: 540 AA.

XX AAE10457: AAE10457 standard; Protein: 540 AA.

XX 18-DEC-2001 (first entry)

XX Human estrogen receptor (ER)-beta protein.

XX Estrogen receptor beta; dietary compound; environmental pollutant;

XX red wine; ER-beta mediated cell growth inhibition modulator; human.

XX Homo sapiens.

XX W0200169262-A1.

XX 20-SEP-2001.

XX 15-MAR-2001: 2001w-0808276.

XX 15-MAR-2001: 2000us-189605P.

XX (DYMA-3) UNIV MASSACHUSETTS.

XX WPI: 2001-546920/67.

XX N-ESTR: AAD18442.

XX In vitro screening for modulation of estrogen receptor beta-mediated

XX cell growth inhibition by contacting cell having functional ER-beta

XX protein with candidate compound and detecting ER-beta regulated gene

XX expression

XX Example 2, Fig 7A; 49pp; English.


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18 001. 1999-142852/12.
XX (UYA ) UNIV YALE.
F1 Human oestrogen receptor beta-4 - useful in treating and monitoring
XX tumours
XX Example 2: Fig 2b; 89pp; English.
XX
07 The present sequence is alternatively spliced isoform mER beta 2
08 of the murine complete oestrogen receptor-beta (ER beta-c) or
09 mER beta-3). The mER beta 3 gene (see AAX24935) contains 9 exons,
10 including the newly described exon 5B, which is not found in ER
11 beta-1. Exon 5B is located in the ligand binding domain of mER
12 beta-3, and probably plays a significant role in mER beta-3 function.
13 The mER beta-2 clone was isolated from an embryonic stem cell
14 genomic library (see exon 3, 2 other isoforms, mER beta 1
15 (see AAW98125) and rat ER beta 4 (see AAW98127), have also been
16 isolated, and the human exon 5B region (see AAX24934) has been
17 identified. Based on these sequences, the invention provides
18 methods for identifying agents that block or augment ER beta-c
19 mediated transcriptional regulation, methods to determine whether
20 ER beta-c or its isoforms is being expressed in tissues or cells,
21 and methods of identifying and using agents that block the
22 transcriptional regulation of genes by ER beta-3 or its isoforms,
23 which in turn modulates other biological and pathological
24 processes. Gene therapy expression of ER beta-c is envisaged.
XX
XX Sequence 510 AA:
SQ
Query Match 94.0%; Score 1119; DB 20; Length 510;
Post local similarity 92.7%; Prot No 36-114;
Matches 216; Conservative 10; Mismatches 7; Indels 0; Gaps 0;
07 1 LVTLTFAEPPIVLTSPSAPFTASMMNSIKIAKEIVHMTSWAKIPGVPISEFQ 60
08 ITTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
09 218 TLTTLTGCTFCTVCTFCTFCTASMMSTLADKLTLTMGWAHKLPGFVLSLIDQ 107
07 61 VLLTSCMVEYLMKIMKSTIDHPKILPAPDYLMDRKCYGVGILFDMILATSP 120
08 ITTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
09 200 TLTTLTGCTFCTVCTFCTFCTASMMSTLADKLTLTMGWAHKLPGFVLSLIDQ 167
07 121 PEIKLQHEVEYCVAMTINSNMPVLTATGTAUSPEKIALI NAVTDAVWVIAKSGIS 180
08 ITTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
09 428 EITTEITLTIEMTSHVETLSEKIMDGLTGVKAKGVPGYSLILEMILAHV 180
07 181 SQQGSMLANIMT SVIVIASKGMKMTIMKROKNVPVYDILLENLNAHV 233
08 ITTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
09 428 EITTEITLTIEMTSHVETLSEKIMDGLTGVKAKGVPGYSLILEMILAHV 180
XX
XX RESULT 14
XX ID AAY04125 standard; Protein: 549 AA
XX AAAY04125.
XX
XX 21 JUN-1999 (first entry)
XX
XX Mouse oestrogen receptor beta isoform mER beta-1.
XX
XX Oestrogen receptor; ER beta-1; ER beta-c; mouse; tumour;
XX diagnosis; therapy; isoform.
XX
XX Mus musculus.
XX
XX W09905170 A1.
XX
XX 04-FEB-1999.
XX
XX 28-JUL-1998; 98W01-0515539.
XX
XX 30-JUL-1997; 97US-0054210.
XX
XX 28-JUL-1997; 97US-0053869.

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XX
XX (UYA ) UNIV YALE.
XX PA Denton R, Fraston C, Gallen R, Rische-Ridon M;
XX F1 Denton R, Fraston C, Gallen R, Rische-Ridon M;
XX Example 2: Fig 2a; 89pp; English.
XX
XX The present sequence is alternatively spliced isoform mER beta-1
XX of the murine complete oestrogen receptor-beta (ER beta-c) or
XX mER beta-3). The mER beta-3 gene (see AAX24935) contains 9 exons,
XX including the newly described exon 5B, which is not found in ER
XX beta-1. Exon 5B is located in the ligand binding domain of mER
XX beta-3, and probably plays a significant role in mER beta-3 function.
XX The mER beta-1 clone was isolated by PCR of mRNA, and by
XX amplification from a mouse embryonic stem cell genomic DNA library.
XX It lacks exon 5B. Preliminary data indicate that the mER beta-1
XX isoform may be more active than the full-length mER beta-3 (see
XX AAW98128). 2 Other isoforms, mER beta 2 (see AAW98126) and rat ER
XX beta-4 (see AAX24934) have also been isolated, and the human exon 5B
XX region (see AAX24934) has been identified. Based on these sequences,
XX the invention provides methods for identifying agents that block or
XX augment ER beta-c mediated transcriptional regulation, methods to
XX determine whether ER beta-c or its isoforms is being expressed in
XX tissues or cells, and methods of identifying and using agents that
XX block the transcriptional regulation of genes by ER beta-c or its
XX isoforms, which in turn modulates other biological and pathological
XX processes. Gene therapy expression of ER beta-c is envisaged.
XX
XX Sequence 549 AA:
SQ
Query Match 94.0%; Score 1119; DB 20; Length 549;
Post local similarity 92.7%; Prot No 36-114;
Matches 216; Conservative 10; Mismatches 7; Indels 0; Gaps 0;
07 1 LVTLTFAEPPIVLTSPSAPFTASMMNSIKIAKEIVHMTSWAKIPGVPISEFQ 60
08 ITTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
09 287 TLTTLTGCTFCTVCTFCTFCTASMMSTLADKLTLTMGWAHKLPGFVLSLIDQ 146
07 61 VLLTSCMVEYLMKIMKSTIDHPKILPAPDYLMDRKCYGVGILFDMILATSP 120
08 ITTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
09 347 TLTTLTGCTFCTVCTFCTFCTASMMSTLADKLTLTMGWAHKLPGFVLSLIDQ 196
07 121 PEIKLQHEVEYCVAMTINSNMPVLTATGTAUSPEKIALI NAVTDAVWVIAKSGIS 180
08 ITTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
09 407 TLTTLTGCTFCTVCTFCTFCTASMMSTLADKLTLTMGWAHKLPGFVLSLIDQ 166
07 181 SQQGSMLANIMT SVIVIASKGMKMTIMKROKNVPVYDILLENLNAHV 233
08 ITTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
09 467 EITTEITLTIEMTSHVETLSEKIMDGLTGVKAKGVPGYSLILEMILAHV 180
XX
XX RESULT 17
XX ID AAY04434 standard; Protein: 549 AA.
XX AAAY04434.
XX
XX 25 JUN 1999 (first entry)
XX
XX Murine mER beta-1 clone protein sequence.
XX
XX Oestrogen receptor beta; oestrogen receptor beta; ER beta.
XX
XX Mus sp.
XX
XX W09905171-A1.

```


KM estrogen receptor mediated disease; complex; ligand antagonist;
 XX Homo sapiens;
 XX OS6228990-B1;
 XX 08 MAY-2001;
 XX 12-FEB-1999; 9408-0249645;
 XX 13-FEB-1998; 9608-0003072;
 XX (KARA) KARA Hiro AB;
 XX Bjornaren J, Thorsell A, Engstrom O, Bonn T, Carlquist M;
 XX Brzezowski AM, Pilewicz AW, Holthoff HF;
 XX W01: 2001-416591/44;
 XX Abstracts comprising amino acids of the estrogen-receptor beta ligand
 XX binding domain complexed with an antagonistic ligand, useful for the
 XX treatment of estrogen receptor mediated diseases in females;
 XX Claim 6; Column 9-12; 21pp; English.

The invention relates to crystals comprising at least 150 amino acid
 residues of the estrogen receptor beta (ERbeta) ligand binding domain
 complexed with a ligand which is an antagonist or partial antagonist.
 The crystals may be used for inhibiting the activity of estradiol
 (or mimetics) by providing ligands which bind to ERbeta with a high
 affinity, blocking the activity of estradiol. Alternatively, binding of
 the ligand to ERbeta may cause conformational changes to ERbeta, thus
 inhibiting further binding to it. Therefore, the ligands are useful in
 the treatment of estrogen receptor mediated diseases in females.
 The present sequence is the protein sequence of a crystal of human
 ERbeta ligand binding domain complexed with agonestien.

Sequence: 229 AA;

Query Match 92.4%; Score 1091.5; DB 20; Length 229;
 Best Local Similarity 94.8%; Prev. No. 1 to 112;
 Matches 221; Conservative 0; Mismatches 1; Indels 11; Gaps 2;

QY 1 LVLLLEAFPPHVIISRAAFTEASMMMSITKAIKEIVIMISWAKITSPVLSIFV 60
 DB |||||||
 QY 6 LVLLLEAFPPHVIISRAAFTEASMMMSITKAIKEIVIMISWAKITSPVLSIFV 62
 DB |||||||
 QY 61 VLLLESTWMEVIMMGLMRSITPHCKLIFADIVLDRCKGCVGELLEFDMLATISRE 120
 DB |||||||
 QY 63 VLLLESTWMEVIMMGLMRSITPHCKLIFADIVLDRCKGCVGELLEFDMLATISRE 122
 DB |||||||
 QY 121 RELKQIKREYLVKAMILINSSMEELVATQIAVSSKNIAHLINAVLDAIWWIVANSGIS 180
 DB |||||||
 QY 122 RELKQIKREYLVKAMILINSSMEELVATQIAVSSKNIAHLINAVLDAIWWIVANSGIS 176
 DB |||||||
 QY 141 SQGSGMPLANILMLISHVHASNKGMHELLNMGCKNVVYVDLLEENLNAVH 234
 DB |||||||
 QY 177 SQGSGMPLANILMLISHVHASNKGMHELLNMGCKNVVYVDLLEENLNAVH 229
 DB |||||||

RESULT 20

AAV4443
ID AAV4443 standard; Protein: 560 AA.

XX AAV04443;

XX 25-JUN-1999 (first entry)

XX Mouse mER beta-3 clone protein sequence.

XX Estrogen receptor beta; estrogen receptor beta; ER beta.

OS Mus sp.
 XX W09905171-A1;
 XX 04-FEB-1999;
 XX 28-JUL-1998; 98WD-0515540;
 XX 30-JUL-1997; 97US-0054210;
 XX 28-JUL-1997; 97US-0054865;
 XX (UYVA) UNIV YALE;
 XX Baron R, Chambon P, Benton R, Dupont S, Garnier J;
 XX W01: 1999-14-675/12;
 XX N-PSDB: AAX33382;
 XX Novel murine estrogen receptor beta genes and splice variants
 XX useful for treating estrogen receptor-beta mediated disorders
 XX Claim 9; Fig 1b-1; 89pp; English.

The present sequence is the murine complete estrogen receptor beta
 (mER beta c) also designated mER beta-3). The protein can be used to
 screen for agents that modulate or block the interaction between the
 ER beta c protein and phytoestrogen, stilbene or triphenylethylene
 (anti)estrogens. The antibody which binds the protein can be used in
 assays to detect activation of the ER beta protein and can be used for
 subcellular localisation of the protein. The complementary nucleic acid
 can be used to inhibit expression of the ER beta c nucleic acid.

Sequence: 560 AA;

Query Match 92.4%; Score 1091; DB 20; Length 560;
 Best Local Similarity 86.1%; Prev. No. 4,46-112;
 Matches 216; Conservative 10; Mismatches 7; Indels 18; Gaps 1;

QY 1 LVLLLEAFPPHVIISRAAFTEASMMMSITKAIKEIVIMISWAKITSPVLSIFV 60
 DB |||||||
 QY 287 LVLLLEAFPPHVIISRAAFTEASMMMSITKAIKEIVIMISWAKITSPVLSIFV 46
 DB |||||||
 QY 61 VLLLESTWMEVIMMGLMRSITPHCKLIFADIVLDRCKGCVGELLEFDMLATISRE 102
 DB |||||||
 QY 347 VLLLESTWMEVIMMGLMRSITPHCKLIFADIVLDRCKGCVGELLEFDMLATISRE 406
 DB |||||||
 QY 103 VLLLESTWMEVIMMGLMRSITPHCKLIFADIVLDRCKGCVGELLEFDMLATISRE 142
 DB |||||||
 QY 407 VLLLESTWMEVIMMGLMRSITPHCKLIFADIVLDRCKGCVGELLEFDMLATISRE 466
 DB |||||||
 QY 121 RELKQIKREYLVKAMILINSSMEELVATQIAVSSKNIAHLINAVLDAIWWIVANSGIS 222
 DB |||||||
 QY 467 RELKQIKREYLVKAMILINSSMEELVATQIAVSSKNIAHLINAVLDAIWWIVANSGIS 226
 DB |||||||
 QY 223 LLEENLNAVH 234
 DB |||||||
 QY 527 LLEENLNAVH 537
 DB |||||||

RESULT 21

AAV98128
ID AAV98128 standard; Protein: 567 AA.

XX AAV98128;

XX 21-JUN-1999 (first entry)

XX Mouse complete estrogen receptor beta mER beta 3.

XX Estrogen receptor; ER beta 3; ER beta c; mouse; tumour;

XX

KESSLER 27

AAH514192

ii) AAI61499 standard; protein: 457 AA.

 $\Delta_{\text{AI}56,1499}^{\circ}$

04 APR-2001 (first entry)

protein encoded by human estrogen receptor alpha isoform #2.

KW Human, estrogen receptor alpha, (cancer, osteoporosis); bone;
 KW Alzheimers; cardiovascular

ANALYTICAL SERVICES, INC.

Homotopy types

WJ20716-ALIN

14 JAN 2001

27-JUN-2000; 2000WB-FR05981.

U.S. AIR FORCE 96140433.

(FILM-) FIKR, MOLEKULAR BIOLOGY LAB.

EL GUARION F., Denoyer S., Flouriot G.

WPI; 2001-137955/24.

Need isomers of human estrogen receptor alpha useful for preparing

Endocrine and cardiovascular diseases

TS Claim 4; Page 46-48; 53pp; English.

CC The present invention relates to a

CC the estrogen receptor are useful for the preparation of therapeutic agents for treating cancer, especially endometrial cancer.

CC Alzheimer's disease and cardiovascular diseases.
XX

Sequence 457 AA:

64 38 - \$6000 7500 00 33

Best local similarity 60.28; Pred. No. 2.1e 75,
Model of 110. Conservatism 54 Misclassification 36

WILLIAMS

| Query Match | Score | DB 22 | Length |
|-------------|-------|-------|--------|
| 64.38 | 759 | | 457 |

Best Local Similarity 60.28; Pred. NO. 2.1e 75,
Model NO. 143; Consistent No. 54; Misnot-bas 36
Total = 1000

Matches 44, Conservatives 54, Mismatches 36, Indels 4, Gaps 3,

[illegible]

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ROYAL
ANTHROPOLOGICAL
INSTITUTE

ААН 46,68%

AAH36684 standard; protein: 480 AA

Δ₁: ΔAB = 66084.

| | |
|----|--|
| DT | 15-MAR-2001 (first entry) |
| XX | |
| DE | Mammalian two-hybrid protein SEQ ID NO:8. |
| XX | |
| KW | Mammalian, two hybrid assay, hybrid protein, hybrid gene, detection, |
| KW | reporter gene; DNA-binding region; transcriptional activation; |
| KW | fused protein; protein interaction. |
| XX | |
| OS | Mammalia. |
| OS | Synthetic. |
| XX | |
| XX | W0200071743-A1. |
| XX | |
| PN | 30-NOV-2000. |
| XX | |
| PP | 25-MAY-2000; 2000MO-JP03354. |
| XX | |
| PR | 25-MAY-1999; 99JP-0144946. |
| XX | |
| PA | (EISA) EISAI CO LTD. |
| XX | |
| E1 | Tsukahara K, Hida T, Nakamura K, Yoshitomi H; |
| XX | |
| XX | WPI, 2001 025163/03. |
| XX | |
| DR | N-PSDB; AAC08199. |
| XX | |
| PT | Report two hybrid detection method comprising fusing two proteins with a |
| PT | DNA binding sequence and a transcription activation sequence |
| PT | respectively for detecting interaction of the proteins in mammalian |
| PT | cells . |
| XX | |
| ES | Example 2, Page 35-37, 64pp, Japanese. |
| XX | |
| CC | The present invention describes a method for detecting the interaction |
| CC | of a first and a second protein within a mammalian cell. The method |
| CC | comprises a fusion protein of the first protein with two or more |
| CC | transcription activation sequences (which may be the same or different), |
| CC | and a fusion protein of the second protein with a DNA binding sequence. |
| CC | These are expressed in a mammalian cell containing DNA carrying a |
| CC | reporter gene downstream of a sequence binding to the DNA-binding |
| CC | sequence, and the expression of the reporter gene is detected to |
| CC | indicate interaction of the two proteins. The method is useful for the |
| CC | identification and examination of protein interactions within the |
| CC | mammalian cell, and screening of potential drugs targeting them. |
| CC | The present sequence represents a hybrid protein from an example given |
| CC | in the present invention. |
| XX | |
| SD | Sequence 480 AA: |

XX

Sequence 480 AA;

| Query Match | 54.38% | Score 759 | 19.22 | Length 480 |
|-----------------------|--------|--|---------|---------------|
| Host Local Similarity | 60.28% | Prod. No. 2.36-755 | | |
| Matches | 142 | Conservative | 51 | Mismatches 26 |
| | | | 1:1:1:1 | 4: 1:1:1 |
| 07 | 1 | LVLLLELLEPRVWVLSK--PSAPVLEASNNKSLKLAFLKLVNMSWQKSLKQVLSLSP | 58 | |
| DE | 1 | LVLLLELLEPRVWVLSK--PSAPVLEASNNKSLKLAFLKLVNMSWQKSLKQVLSLSP | 58 | |
| DE | 184 | LVLLLELLEPRVWVLSK--PSAPVLEASNNKSLKLAFLKLVNMSWQKSLKQVLSLSP | 242 | |
| 07 | 55 | LVVLLLESLNMLVIMNQLKMSKFLDHLGKLFALFVLSNLSKLVNGLVLEPRVLTATIS | 118 | |
| DE | 243 | LVVLLLESLNMLVIMNQLKMSKFLDHLGKLFALFVLSNLSKLVNGLVLEPRVLTATIS | 402 | |
| 07 | 119 | FFSTFKLQHEPRVQVWAMLLNSQWYVLTATQFASNNKSLKLLHNAVIVLVWVLSK | 177 | |
| DE | 303 | FFSTFKLQHEPRVQVWAMLLNSQWYVLTATQFASNNKSLKLLHNAVIVLVWVLSK | 462 | |
| 07 | 178 | GLSSQSGSMRLANLMLKSLSVNRSKQWENLLNRKCKNVAVVVDLLDPMNAIVL | 234 | |
| DE | 363 | GLSSQSGSMRLANLMLKSLSVNRSKQWENLLNRKCKNVAVVVDLLDPMNAIVL | 418 | |

RESULT 29

AAY21626

QY 61 CYEWM 66
 D6 92 CYEWM 97

RESULT 2

Q9H0M5 PRELIMINARY: PRT: 486 AA.
 AC Q9H0M5
 DT 01 DEC 2001 (TREMUR-19, created)
 DT 01 DEC 2001 (TREMUR-19, last sequence update)
 DT 01 DEC 2001 (TREMUR-19, last annotation update)
 DE ESTROGEN RECEPTOR BETA 2.
 OS Gallitrix jaculus (Common murrelet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Platyrrhini; Platyrrhini; Gallitridae; Gallitrix.
 NX NCBI TaxID 9483.
 RN 111
 RP SEQUENCE FROM N.A.
 RA Scobie C.A., Wilson J.A., Millar M.R., Macpherson S., Saunders P.T.:
 RT "The estrogen receptor beta variant ERbeta v2/ERbeta2 is expressed in
 RT a wide range of tissues in both old and New World primates."
 RL Submitted (JUN 2001) to the EMBL/GenBank/DDBJ databases.
 LR EMBL: AF034816; AAK7148.1;
 KW Receptor.
 SQ SEQUENCE: 486 AA: 54144 MW: 4829.0837 3711277 CIRC4;

Query Match: 100.0%; Score: 486; DB 6; Length: 486;
 Best Local Similarity: 100.0%; Prod. No.: 4, 86-42;
 Matches: 66; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 1 CAVSIVASCYHYVWS-TEKAKFKRKSLGHNLYTVAIINQTIQKNEPSSVAWTLR 60
 D6 149 CAVSIVASCYHYVWS-TEKAKFKRKSLGHNLYTVAIINQTIQKNEPSSVAWTLR 208
 QY 61 CYEWM 66
 D6 209 CYEWM 214

RESULT 4
 Q91ZB6 PRELIMINARY: PRT: 503 AA.

AC Q91ZB6
 DT 01 DEC 2001 (TREMUR-19, created)
 DT 01 DEC 2001 (TREMUR-19, last sequence update)
 DT 01 DEC 2001 (TREMUR-19, last annotation update)
 DE ESTROGEN RECEPTOR BETA TYPE II (BETA VARIANT).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NX NCBI TaxID 10090.
 RN 111
 RP SEQUENCE FROM N.A.
 RA Baum Z., van Boven J.P., Karpman M., Papapanagos S., Jewik C.:
 RT "Expression of KSA4 cells to estrogen enhancers estrogenic and
 RT inhibits adipogenesis."
 RL J. Bone Miner. Res. 010 (2001).
 LR EMBL: AF034413; AAK5175.1;
 KW Receptor.
 SQ SEQUENCE: 503 AA: 56372 MW: 5635.0831 403271 CIRC54;

Query Match: 100.0%; Score: 486; DB 11; Length: 503;
 Best Local Similarity: 100.0%; Prod. No.: 4, 86-42;
 Matches: 66; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 1 CAVSIVASCYHYVWS-TEKAKFKRKSLGHNLYTVAIINQTIQKNEPSSVAWTLR 60
 D6 104 CAVSIVASCYHYVWS-TEKAKFKRKSLGHNLYTVAIINQTIQKNEPSSVAWTLR 163

QY 61 CYEWM 66
 D6 164 CYEWM 169

RESULT 4

Q9H0M5 PRELIMINARY: PRT: 526 AA.
 AC Q9H0M5
 DT 01 JUN 2001 (TREMUR-17, created)
 DT 01 JUN 2001 (TREMUR-17, last sequence update)
 DT 01 DEC 2001 (TREMUR-19, last annotation update)
 DE ESTROGEN RECEPTOR BETA.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Eumetazoa; Platyrrhini; Suidae; Sus.
 NX NCBI TaxID 9823.
 RN 111
 RP SEQUENCE FROM N.A.
 RA Lavoie B.A., Deslorme D.C.:
 RT "Cloning and expression of estrogen receptor beta isoforms from
 RT porcine ovary."
 RL Endocrinology 0:0-0(2000).
 CC -1. SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
 LR EMBL: AF267746; AAK5151.1;
 KW HSPD; P03472; HRCV.
 DR InterPro: IP0000546; hormone_rec_114.
 DR InterPro: IP001724; steroid_hormone_receptor.
 DR InterPro: IP001628; z1-c4.
 DR Pfam: PF00104; hormone_rec_1.
 DR Pfam: PF00105; z1-c4_1.
 DR PRINTS: PR00199; STRODERM-INT.
 DR PRINTS: PR00047; STRODERM-INT.
 DR SMART: SM00430; HOL1_1.
 DR SMART: SM00399; ZNF_C4_1.
 DR PROSITE: PS00031; NUCLEAR_RECEPTOR_1.
 KW DNA-binding; Nuclear protein; Receptor; Transcription regulation;
 KW Zinc-finger.
 SQ SEQUENCE: 526 AA: 58647 MW: 44036.7021 18146 CIRC44;

Query Match: 100.0%; Score: 486; DB 6; Length: 526;
 Best Local Similarity: 100.0%; Prod. No.: 4, 86-42;
 Matches: 66; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 1 CAVSIVASCYHYVWS-TEKAKFKRKSLGHNLYTVAIINQTIQKNEPSSVAWTLR 60
 D6 146 CAVSIVASCYHYVWS-TEKAKFKRKSLGHNLYTVAIINQTIQKNEPSSVAWTLR 205
 QY 61 CYEWM 66
 D6 206 CYEWM 211

RESULT 5

Q9H0M5 PRELIMINARY: PRT: 553 AA.
 AC Q9H0M5
 DT 01 JUN 2001 (TREMUR-17, created)
 DT 01 JUN 2001 (TREMUR-17, last sequence update)
 DT 01 DEC 2001 (TREMUR-19, last annotation update)
 DE ESTROGEN RECEPTOR BETA.
 OS Brachycaudus rostratus (Zebrafinch).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Cyprinodontiformes; Poeyaceae; Brachycaudinae; Brachycaudini;
 OC Cyprinodontiformes; Cyprinodontiformes; Brachycaudini.
 NX NCBI TaxID 79557.
 RN 111
 RP SEQUENCE FROM N.A.


```

146 212 CYEWM 210
RESULT 9
AC G983M9 PRELIMINARY: PRT: 569 AA.
AC G983M9
01 01 JUN 2001 (REMOVED: 17, created)
01 01 JUN 2001 (REMOVED: 17, last sequence update)
01 01 DEC 2001 (REMOVED: 19, last annotation update)
06 ESTROGEN RECEPTOR ALPHA.
06 brachydanio rerio (Zebrafish) (Zebra danio).
06 Eukaryotic Metazoa: Chordata: Vertebrata: Euteleostomi:
06 Actinopterygii: Neopterygii: Teleostei: Euteleostei: Ostariophysi:
06 Cyprinodontes: Cyprinodontes: Danio.
06 NCBI Taxid 7955.
06 111
06 SEQUENCE FROM N.A.
06 TISSUE LIVER.
06 AKRON B.C. KISHIDA M., Callard G.V.
06 *Testes from receptor cDNAs in zebrafish.*
06 Submitted (FEB 2001) to the EMBL/GenBank/DDBJ databases.
06 1 SHELLHARKE LOCATIONS: NORTON (BY SIMILARITY).
06 EMBL: AF445412; AKR16740.1.
06 HESTY: J03472; HET.
06 InterPro: IPR000566; Hormone_rec_1b.
06 InterPro: IPR001292; test_recep.
06 InterPro: IPR001253; Steroid_hormone_receptor.
06 InterPro: IPR001628; Z1_c4.
06 ELM: P900104; Hormone_rec_1.
06 ELM: P902159; test_recep_1.
06 ELM: P900109; Z1_c4_1.
06 PESTS: PEST198; STRONGESTS.
06 PESTS: IPR000473; STRONGESTS.
06 SMART: SM00399; Znf_c4_1.
06 SMART: SM00399; Znf_c4_1.
06 Protein: P500043; NUTLAR RECEPTOR 1.
06 DNA binding: No local proteins accepted. Transcription required.
06 KW Zinc Finger.
06 SEQUENCE: 569 AA: 6286 MW: 674014.6765 kDa CR644.

Query Match 99.0% Score 482; DB 15 Length 569;
Best Local Similarity 97.0% Prod. No. 15641;
Matches 64; Conserved 2; Mismatches 0; Indels 0; Gaps 0.

147 212 CYEWM 211
RESULT 10
AC G983M9 PRELIMINARY: PRT: 620 AA.
AC G983M9
01 01 DEC 2001 (REMOVED: 19, created)
01 01 DEC 2001 (REMOVED: 19, last sequence update)
01 01 DEC 2001 (REMOVED: 19, last annotation update)
06 ESTROGEN RECEPTOR ALPHA.
06 clarias gariepinus (Sharptooth catfish) (African catfish).
06 Eukaryotic Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
06 Actinopterygii: Neopterygii: Teleostei: Euteleostei: Ostariophysi:
06 Siluriformes: Clariidae: Clarias.
06 NCBI Taxid 10013.
06 111
06 SEQUENCE FROM N.A.
06 TISSUE TESTIS.
06 JACOBS J.D., Bedford J.

```

```

06 111
06 SEQUENCE FROM N.A.
06 TISSUE LIVER.
06 AKRON B.C. KISHIDA M., Callard G.V.
06 *Testes from receptor cDNAs in zebrafish.*
06 Submitted (FEB 2001) to the EMBL/GenBank/DDBJ databases.
06 1 SHELLHARKE LOCATIONS: NORTON (BY SIMILARITY).
06 EMBL: AF445412; AKR16740.1.
06 HESTY: J03472; HET.
06 InterPro: IPR000566; Hormone_rec_1b.
06 InterPro: IPR001292; test_recep.
06 InterPro: IPR001253; Steroid_hormone_receptor.
06 InterPro: IPR001628; Z1_c4.
06 ELM: P900104; Hormone_rec_1.
06 ELM: P902159; test_recep_1.
06 ELM: P900109; Z1_c4_1.
06 PESTS: PEST198; STRONGESTS.
06 PESTS: IPR000473; STRONGESTS.
06 SMART: SM00399; Znf_c4_1.
06 SMART: SM00399; Znf_c4_1.
06 Protein: P500043; NUTLAR RECEPTOR 1.
06 DNA binding: No local proteins accepted. Transcription required.
06 KW Zinc Finger.
06 SEQUENCE: 569 AA: 6286 MW: 674014.6765 kDa CR644.

Query Match 99.0% Score 482; DB 15 Length 569;
Best Local Similarity 97.0% Prod. No. 15641;
Matches 64; Conserved 2; Mismatches 0; Indels 0; Gaps 0.

148 212 CYEWM 212
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01 01 DEC 2001 (REMOVED: 19, last sequence update)
01 01 DEC 2001 (REMOVED: 19, last annotation update)
06 ESTROGEN RECEPTOR ALPHA.
06 brachydanio rerio (Zebrafish) (Zebra danio).
06 Eukaryotic Metazoa: Chordata: Vertebrata: Euteleostomi:
06 Actinopterygii: Neopterygii: Teleostei: Euteleostei: Ostariophysi:
06 Cyprinodontes: Cyprinodontes: Danio.
06 NCBI Taxid 7955.
06 111
06 SEQUENCE FROM N.A.
06 TISSUE LIVER.
06 AKRON B.C. KISHIDA M., Callard G.V.
06 *Testes from receptor cDNAs in zebrafish.*
06 Submitted (FEB 2001) to the EMBL/GenBank/DDBJ databases.
06 1 SHELLHARKE LOCATIONS: NORTON (BY SIMILARITY).
06 EMBL: AF445412; AKR16740.1.
06 HESTY: J03472; HET.
06 InterPro: IPR000566; Hormone_rec_1b.
06 InterPro: IPR001292; test_recep.
06 InterPro: IPR001253; Steroid_hormone_receptor.
06 InterPro: IPR001628; Z1_c4.
06 ELM: P900104; Hormone_rec_1.
06 ELM: P902159; test_recep_1.
06 ELM: P900109; Z1_c4_1.
06 PESTS: PEST198; STRONGESTS.
06 PESTS: IPR000473; STRONGESTS.
06 SMART: SM00399; Znf_c4_1.
06 SMART: SM00399; Znf_c4_1.
06 Protein: P500043; NUTLAR RECEPTOR 1.
06 DNA binding: No local proteins accepted. Transcription required.
06 KW Zinc Finger.
06 SEQUENCE: 569 AA: 6286 MW: 674014.6765 kDa CR644.

Query Match 99.0% Score 480; DB 6 Length 249;
Best Local Similarity 97.0% Prod. No. 15641;
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01 01 NOV 1996 (REMOVED: 01, last sequence update)
01 01 DEC 2001 (REMOVED: 19, last annotation update)
06 ESTROGEN RECEPTOR-RELATED PROTEIN.

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| QY | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 | 46 | 47 | 48 | 49 | 50 | 51 | 52 | 53 | 54 | 55 | 56 | 57 | 58 | 59 | 60 | 61 | 62 | 63 | 64 | 65 | 66 | 67 | 68 | 69 | 70 | 71 | 72 | 73 | 74 | 75 | 76 | 77 | 78 | 79 | 80 | 81 | 82 | 83 | 84 | 85 | 86 | 87 | 88 | 89 | 90 | 91 | 92 | 93 | 94 | 95 | 96 | 97 | 98 | 99 | 100 |
|----|---|---|---|---|---|---|---|---|---|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|-----|
| QY | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 | 46 | 47 | 48 | 49 | 50 | 51 | 52 | 53 | 54 | 55 | 56 | 57 | 58 | 59 | 60 | 61 | 62 | 63 | 64 | 65 | 66 | 67 | 68 | 69 | 70 | 71 | 72 | 73 | 74 | 75 | 76 | 77 | 78 | 79 | 80 | 81 | 82 | 83 | 84 | 85 | 86 | 87 | 88 | 89 | 90 | 91 | 92 | 93 | 94 | 95 | 96 | 97 | 98 | 99 | 100 |
| QY | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 | 46 | 47 | 48 | 49 | 50 | 51 | 52 | 53 | 54 | 55 | 56 | 57 | 58 | 59 | 60 | 61 | 62 | 63 | 64 | 65 | 66 | 67 | 68 | 69 | 70 | 71 | 72 | 73 | 74 | 75 | 76 | 77 | 78 | 79 | 80 | 81 | 82 | 83 | 84 | 85 | 86 | 87 | 88 | 89 | 90 | 91 | 92 | 93 | 94 | 95 | 96 | 97 | 98 | 99 | 100 |
| QY | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 | 46 | 47 | 48 | 49 | 50 | 51 | 52 | 53 | 54 | 55 | 56 | 57 | 58 | 59 | 60 | 61 | 62 | 63 | 64 | 65 | 66 | 67 | 68 | 69 | 70 | 71 | 72 | 73 | 74 | 75 | 76 | 77 | 78 | 79 | 80 | 81 | 82 | 83 | 84 | 85 | 86 | 87 | 88 | 89 | 90 | 91 | 92 | 93 | 94 | 95 | 96 | 97 | 98 | 99 | 100 |
| QY | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 | 46 | 47 | 48 | 49 | 50 | 51 | 52 | 53 | 54 | 55 | 56 | 57 | 58 | 59 | 60 | 61 | 62 | 63 | 64 | 65 | 66 | 67 | 68 | 69 | 70 | 71 | 72 | 73 | 74 | 75 | 76 | 77 | 78 | 79 | 80 | 81 | 82 | 83 | 84 | 85 | 86 | 87 | 88 | 89 | 90 | 91 | 92 | 93 | 94 | 95 | 96 | 97 | 98 | 99 | 100 |
| QY | 1 | 2 | 3 | 4 | 5 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |


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105 Homo sapiens (Human)
106 Tokuyasu A. Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
107 Placentalia: Eutheria: Primates: Catarrhini: Hominoidea: Homo.
108 NCBI TaxID 9606;
109 [1]
110 SEQUENCE FROM N.A.
111
112 TITLE TESTS:
113 REFID: 9658945, PubMed 244376.
114
115 Chazotte M.V.:
116 "Specific region in hormone binding domain is essential for hormone
117 binding and trans activation by human androgen receptor."
118 Mol. Endocrinol. 4:417-427(1990).
119
120 1. SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
121 2. SIMILARITY BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
122 EMBL: M00099; AAA1745.1;
123
124 HSS: 906546; 100%.
125
126 InterPro: IP001103; Androgen_recep.
127 InterPro: IP000566; Hormone_rec_119.
128 InterPro: IP001628; Z1_C4;
129 Pfam: PF02166; Androgen_recep_1.
130 Pfam: PF00104; hormone_rec_1.
131 Pfam: PF00105; Z1_C4; 1.
132 PRINTS: PR00047; STROLDINCR.
133 SMART: SM00400; bHLH_1.
134 SMART: SM00499; ZNF_C4; 1.
135 PROSITE: PS00041; NUCLEAR_RECEP08; 1.
136 DNA Binding: Nuclear protein, receptor; Transcription regulation;
137 Zinc finger.
138
139 SIGNATURE: 740 AA; 79150 MW; 91884748410009 cko64;
140
141 Query Match: 61.9%; Score 239; ID 4; Length 740;
142 best local similarity: 59.1%; Prod. No. 846-23;
143 Matches: 49; Conserved: 9; Mismatches: 19; Indels: 0; Gaps: 0;
144
145 QY 1 CAAVSAVSAHYGVMSVLCRAIKRSVGNDAICVATNGLDKMRKSNVAPLR 60
146 I E I I I I I I I I I I I I I I I I I I I I I I I I I I I
147 413 CLIPSDASGVALGALGSKVEFKKAEKCEYLVASINLIDKPPNTPSLR 472
148
149 QY 61 CFEVCM 66
150 I I I I I
151 473 CFEVCM 478
152
153 RESULT 28
154
155 ID 170048 PRELIMINARY: PR2 769 AA.
156
157 DE 01-FEB-1997 (TERMINAL: 08, created)
158 DT 01-JAN-1999 (TERMINAL: 09, last sequence update)
159 DT 01-DEC-2001 (TERMINAL: 19, last annotation update)
160 AB ABSTRACT: Xenopus.
161
162 NCBI TaxID 8359;
163
164 RN [1]
165
166 SEQUENCE FROM N.A.
167 MEDLINE 9382475; PubMed 7601402;
168
169 KA Fischer L.M., Katz D., Kelley D.B.
170 "Androgen-directed development of the Xenopus laevis tail: control
171 of androgen receptor expression and tissue differentiation."
172 Dev. Biol. 170:115-126(1995).
173
174 RN [4]
175
176 SEQUENCE FROM N.A.
177 Kelley D.B., Kamowitz E.R., Kelley D.B., Budya T.C.:
178 Submitted (DEC-1998) to the EMBL/Genbank/DBS databases.
179 1. SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
180 2. SIMILARITY BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
181 EMBL: U67129; AF097866.1;
182
183 HSS: 906546; 100%.
184
185 InterPro: IP001103; Androgen_recep.
186 InterPro: IP000566; Hormone_rec_119.
187 InterPro: IP001628; Z1_C4;
188 Pfam: PF02166; Androgen_recep_1.
189 Pfam: PF00104; hormone_rec_1.
190 Pfam: PF00105; Z1_C4; 1.
191 PRINTS: PR00047; STROLDINCR.
192 SMART: SM00400; bHLH_1.
193 SMART: SM00499; ZNF_C4; 1.
194 PROSITE: PS00041; NUCLEAR_RECEP08; 1.
195 DNA Binding: Nuclear protein, receptor; Transcription regulation;
196 Zinc finger.

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105 Homo sapiens (Human)
106 Tokuyasu A. Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
107 Placentalia: Eutheria: Primates: Catarrhini: Hominoidea: Homo.
108 NCBI TaxID 9606;
109 [1]
110 SEQUENCE FROM N.A.
111
112 TITLE TESTS:
113 REFID: 9658945, PubMed 244376.
114
115 Chazotte M.V.:
116 "Specific region in hormone binding domain is essential for hormone
117 binding and trans activation by human androgen receptor."
118 Mol. Endocrinol. 4:417-427(1990).
119
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124 HSS: 906546; 100%.
125
126 InterPro: IP001103; Androgen_recep.
127 InterPro: IP000566; Hormone_rec_119.
128 InterPro: IP001628; Z1_C4;
129 Pfam: PF02166; Androgen_recep_1.
130 Pfam: PF00104; hormone_rec_1.
131 Pfam: PF00105; Z1_C4; 1.
132 PRINTS: PR00047; STROLDINCR.
133 SMART: SM00400; bHLH_1.
134 SMART: SM00499; ZNF_C4; 1.
135 PROSITE: PS00041; NUCLEAR_RECEP08; 1.
136 DNA Binding: Nuclear protein, receptor; Transcription regulation;
137 Zinc finger.
138
139 SIGNATURE: 740 AA; 79150 MW; 91884748410009 cko64;
140
141 Query Match: 61.9%; Score 239; ID 4; Length 740;
142 best local similarity: 59.1%; Prod. No. 846-23;
143 Matches: 49; Conserved: 9; Mismatches: 19; Indels: 0; Gaps: 0;
144
145 QY 1 CAAVSAVSAHYGVMSVLCRAIKRSVGNDAICVATNGLDKMRKSNVAPLR 60
146 I E I I I I I I I I I I I I I I I I I I I I I I I I I I I
147 413 CLIPSDASGVALGALGSKVEFKKAEKCEYLVASINLIDKPPNTPSLR 472
148
149 QY 61 CFEVCM 66
150 I I I I I
151 473 CFEVCM 478
152
153 RESULT 29
154
155 ID 170048 PRELIMINARY: PR2 790 AA.
156
157 DE 01-FEB-1997 (TERMINAL: 02, created)
158 DT 01-JAN-1999 (TERMINAL: 09, last sequence update)
159 DT 01-DEC-2001 (TERMINAL: 19, last annotation update)
160 AB ABSTRACT: XENOPUS LAEVIS (AFRICAN CLAWED TOAD).
161
162 NCBI TaxID 8359;
163
164 RN [1]
165
166 SEQUENCE FROM N.A.
167 MEDLINE 9382475; PubMed 7601402;
168
169 KA Fischer L.M., Katz D., Kelley D.B.
170 "Androgen-directed development of the Xenopus laevis tail: control
171 of androgen receptor expression and tissue differentiation."
172 Dev. Biol. 170:115-126(1995).
173
174 RN [4]
175
176 SEQUENCE FROM N.A.
177 Kelley D.B., Kamowitz E.R., Kelley D.B., Budya T.C.:
178 Submitted (DEC-1998) to the EMBL/Genbank/DBS databases.
179 1. SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
180 2. SIMILARITY BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
181 EMBL: U67129; AF097866.1;
182
183 HSS: 906546; 100%.
184
185 InterPro: IP001103; Androgen_recep.
186 InterPro: IP000566; Hormone_rec_119.
187 InterPro: IP001628; Z1_C4;
188 Pfam: PF02166; Androgen_recep_1.
189 Pfam: PF00104; hormone_rec_1.
190 Pfam: PF00105; Z1_C4; 1.
191 PRINTS: PR00047; STROLDINCR.
192 SMART: SM00400; bHLH_1.
193 SMART: SM00499; ZNF_C4; 1.
194 PROSITE: PS00041; NUCLEAR_RECEP08; 1.
195 DNA Binding: Nuclear protein, receptor; Transcription regulation;
196 Zinc finger.

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Q7. What is the main message of the book?

DB 284 VELLES'WMEVIMWGLMWSKIDHMKELFAHUVIADDERKCVGILLETEDMLATISRE 442
 07 1.1 VELLES'WMEVIMWGLMWSKIDHMKELFAHUVIADDERKCVGILLETEDMLATISRE 120
 DB 434 VELLES'WMEVIMWGLMWSKIDHMKELFAHUVIADDERKCVGILLETEDMLATISRE 442
 07 1.1 VELLES'WMEVIMWGLMWSKIDHMKELFAHUVIADDERKCVGILLETEDMLATISRE 120
 DB 409 VELLES'WMEVIMWGLMWSKIDHMKELFAHUVIADDERKCVGILLETEDMLATISRE 442

RESULT 4
 US OR 86-620A-14
 1 Sequence 1: Application US/08/06/06
 2 Patent No. 5958710
 3 GENERAL INFORMATION
 4 APPLICANT: WILKINSON, HILARY
 5 TITLE OF INVENTION: DISTROPHIN RECEPTOR
 6 FILING DATE: 08-MAY-1996
 7 PRIORITY DATE: 08-MAY-1996
 8 INVENTION FOR SEQ TO NO: 14
 9 SEQUENCE CHARACTERISTICS
 10 LENGTH: 484 amino acids
 11 TYPE: amino acid
 12 TOPOLOGY: linear
 13 ORIGINAL SOURCE:
 14 ORGANISM: Rattus rattus
 US OR 86-620A-14

Query Match 94.18% Score 1111 DB 4 Length 484
 Post local similarity 94.18% Pred. No. 4.28 12% Mismatches 82 Indels 0 Gaps 0
 Matches 217 Conserved 82 Mismatches 82 Indels 0 Gaps 0

07 1.1 VELLES'WMEVIMWGLMWSKIDHMKELFAHUVIADDERKCVGILLETEDMLATISRE 120
 DB 280 VELLES'WMEVIMWGLMWSKIDHMKELFAHUVIADDERKCVGILLETEDMLATISRE 442
 07 6.1 VELLES'WMEVIMWGLMWSKIDHMKELFAHUVIADDERKCVGILLETEDMLATISRE 120
 DB 434 VELLES'WMEVIMWGLMWSKIDHMKELFAHUVIADDERKCVGILLETEDMLATISRE 442
 07 1.1 VELLES'WMEVIMWGLMWSKIDHMKELFAHUVIADDERKCVGILLETEDMLATISRE 120
 DB 409 VELLES'WMEVIMWGLMWSKIDHMKELFAHUVIADDERKCVGILLETEDMLATISRE 442

07 1.1 VELLES'WMEVIMWGLMWSKIDHMKELFAHUVIADDERKCVGILLETEDMLATISRE 120
 DB 409 VELLES'WMEVIMWGLMWSKIDHMKELFAHUVIADDERKCVGILLETEDMLATISRE 442

RESULT 4
 US OR 86-620A-14
 1 Sequence 1: Application US/08/06/06
 2 Patent No. 5958710
 3 GENERAL INFORMATION
 4 APPLICANT:
 5 TITLE OF INVENTION: orphan receptor
 6 NUMBER OF SEQUENCES: 19
 7 COMPUTER RELEVANCE FORM:
 8 METHOD TYPE: floppy disk
 9 COMPUTER: IBM PC compatible
 10 OPERATING SYSTEM: pc dos/ms dos
 11 SOFTWARE: Patent In Release #1.0, Version #1.25 (GPO)
 12 PRIOR APPLICATION DATA:
 13 APPLICATION NUMBER: US/08/06/06, 620A
 14 FILING DATE:
 15 PRIOR APPLICATION DATA:
 16 APPLICATION NUMBER: US/08/06/06, 620A
 17 FILING DATE:
 18 APPLICATION NUMBER: US/08/06/06, 620A
 19 FILING DATE:

07 FILING DATE:
 08 APPLICATION NUMBER: GB 9618272.1
 09 FILING DATE: 08-SEP-1995
 10 PRIOR APPLICATION DATA:
 11 FILING DATE: 15-MAR-1996
 12 FILING DATE: 15-MAR-1996
 13 FILING DATE: 15-MAR-1996
 14 FILING DATE: 15-MAR-1996
 15 FILING DATE: 15-MAR-1996
 16 FILING DATE: 15-MAR-1996
 17 FILING DATE: 15-MAR-1996
 18 FILING DATE: 15-MAR-1996
 19 FILING DATE: 15-MAR-1996

Query Match 94.18% Score 1111 DB 2 Length 484
 Post local similarity 94.18% Pred. No. 4.28 12% Mismatches 82 Indels 0 Gaps 0
 Matches 217 Conserved 82 Mismatches 82 Indels 0 Gaps 0

07 1.1 VELLES'WMEVIMWGLMWSKIDHMKELFAHUVIADDERKCVGILLETEDMLATISRE 120
 DB 284 VELLES'WMEVIMWGLMWSKIDHMKELFAHUVIADDERKCVGILLETEDMLATISRE 442
 07 6.1 VELLES'WMEVIMWGLMWSKIDHMKELFAHUVIADDERKCVGILLETEDMLATISRE 120
 DB 434 VELLES'WMEVIMWGLMWSKIDHMKELFAHUVIADDERKCVGILLETEDMLATISRE 442
 07 1.1 VELLES'WMEVIMWGLMWSKIDHMKELFAHUVIADDERKCVGILLETEDMLATISRE 120
 DB 409 VELLES'WMEVIMWGLMWSKIDHMKELFAHUVIADDERKCVGILLETEDMLATISRE 442

RESULT 4
 US OR 86-620A-2
 1 Sequence 2: Application US/08/06/06
 2 Patent No. 5958710
 3 GENERAL INFORMATION
 4 APPLICANT:
 5 TITLE OF INVENTION: orphan receptor
 6 NUMBER OF SEQUENCES: 19
 7 COMPUTER RELEVANCE FORM:
 8 METHOD TYPE: floppy disk
 9 COMPUTER: IBM PC compatible
 10 OPERATING SYSTEM: pc dos/ms dos
 11 SOFTWARE: Patent In Release #1.0, Version #1.25 (GPO)
 12 PRIOR APPLICATION DATA:
 13 APPLICATION NUMBER: US/08/06/06, 620A
 14 FILING DATE:
 15 PRIOR APPLICATION DATA:
 16 APPLICATION NUMBER: US/08/06/06, 620A
 17 FILING DATE:
 18 APPLICATION NUMBER: US/08/06/06, 620A
 19 FILING DATE:

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 485 amino acids
TYPE: amino acid
TOPOLOGY: linear
ORIGINAL SOURCE:
ORGANISM: Ratios Tactos
US-08-826-620A 2

Query Match: 94.1% Score 1111, DB 2, Length 485
Post Local Similarity: 94.1% Pred. No. 4,20-123;
Matches 214, Conservative 9, Mismatches 8, Indels 0, Gaps 0

1 LVITLLEAEPPHVLISGRSAFTFASMMSSLTPLAKELVHMLSMARKIDGVHSLPQ 60
|||||
223 LVITLLEAEPPHVLISGRSAFTFASMMSSLTPLAKELVHMLSMARKIDGVHSLPQ 282
61 VLLLESTWMEVLMGIMKSLIDHGRKLEFADQVLDHGRKVEGILHFDMLATTSP 120
|||||
283 VLLLESTWMEVLMGIMKSLIDHGRKLEFADQVLDHGRKVEGILHFDMLATTSP 342
121 PFTLEGGVYLVYAMHLSNSEEETVATLZALSKETLHNAVTAIYVATASGTS 180
|||||
443 PFTLEGGVYLVYAMHLSNSEEETVATLZALSKETLHNAVTAIYVATASGTS 402
141 SGGSSMARIATLSVPLNSGRKMLLDRGRKRVVYDLEMLNARY 233
|||||
403 SGGSSMARIATLSVPLNSGRKMLLDRGRKRVVYDLEMLNARY 455

RESULT 5
US-08-826-620A-14
Sequence 14 Application US-08-826-620A
Patent No. 6958710
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: orphan receptor
NUMBER OF SEQUENCES: 19
COMPUTER RELEASABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25 (EP)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US-08-826-620A
FILING DATE:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 11/2796/03933
FILING DATE:
APPLICATION NUMBER: GB 9518272.1
FILING DATE: 08-SEP-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: GB 9605550.4
FILING DATE: 15-MAR-1996
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: GB 9607532.0
FILING DATE: 11-APR-1996
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: GB 9609576.5
FILING DATE: 08-MAY-1996
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 484 amino acids
TYPE: amino acid
TOPOLOGY: linear
ORIGINAL SOURCE:
ORGANISM: Mus musculus
US-08-826-620A-14

Query Match: 92.5% Score 1093, DB 2, Length 484,
Post Local Similarity: 91.8% Pred. No. 6,16-123;

Matches 214, Conservative 10, Mismatches 9, Indels 0, Gaps 0

22 1 LVITLLEAEPPHVLISGRSAFTFASMMSSLTPLAKELVHMLSMARKIDGVHSLPQ 60
|||||
100 223 LVITLLEAEPPHVLISGRSAFTFASMMSSLTPLAKELVHMLSMARKIDGVHSLPQ 282
61 VLLLESTWMEVLMGIMKSLIDHGRKLEFADQVLDHGRKVEGILHFDMLATTSP 120
|||||
283 VLLLESTWMEVLMGIMKSLIDHGRKLEFADQVLDHGRKVEGILHFDMLATTSP 342
121 PFTLEGGVYLVYAMHLSNSEEETVATLZALSKETLHNAVTAIYVATASGTS 180
|||||
443 PFTLEGGVYLVYAMHLSNSEEETVATLZALSKETLHNAVTAIYVATASGTS 402
141 SGGSSMARIATLSVPLNSGRKMLLDRGRKRVVYDLEMLNARY 233
|||||
403 SGGSSMARIATLSVPLNSGRKMLLDRGRKRVVYDLEMLNARY 455
RESULT 6
US-08-826-620A-5
Sequence 5, Application US-08-826-620A
Patent No. 6958710
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: orphan receptor
NUMBER OF SEQUENCES: 19
COMPUTER RELEASABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25 (EP)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US-08-826-620A
FILING DATE:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 11/2796/03933
FILING DATE:
APPLICATION NUMBER: GB 9518272.1
FILING DATE: 08-SEP-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: GB 9605550.4
FILING DATE: 15-MAR-1996
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: GB 9607532.0
FILING DATE: 11-APR-1996
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: GB 9609576.5
FILING DATE: 08-MAY-1996
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 485 amino acids
TYPE: amino acid
TOPOLOGY: linear
ORIGINAL SOURCE:
ORGANISM: Mus musculus
US-08-826-620A-5

Query Match: 92.5% Score 1093, DB 2, Length 485,
Post Local Similarity: 91.8% Pred. No. 6,20-123;
Matches 214, Conservative 10, Mismatches 9, Indels 0, Gaps 0

61 VLLLESTWMEVLMGIMKSLIDHGRKLEFADQVLDHGRKVEGILHFDMLATTSP 120
|||||
283 VLLLESTWMEVLMGIMKSLIDHGRKLEFADQVLDHGRKVEGILHFDMLATTSP 342
121 PFTLEGGVYLVYAMHLSNSEEETVATLZALSKETLHNAVTAIYVATASGTS 180
|||||

Best Local Similarity: 100.0%; Prod. No. 1.4e-113;
 Post Local Similarity: 93.4%; Prod. No. 1.6e-105;
 Matches: 183; Conservative: 6; Mismatches: 7; Indels: 0; Gaps: 0;

Q7 1 EVTLTFAPIPVVTSPPAPFTASPPMSTTFLAPETVMTSWAPFTQVETLSTLEQ 60
 184 EVTLTFAPIPVVTSPPAPFTASPPMSTTFLAPETVMTSWAPFTQVETLSTLEQ 243
 Q7 61 VVLLTSTVWKEVLMGIMKRSITDQKILFAPDLVLDKQKCVGCHLEFDMLATTSR 120
 244 VVLLTSTVWKEVLMGIMKRSITDQKILFAPDLVLDKQKCVGCHLEFDMLATTSR 303
 Q7 121 RELFTVHSEVTVVAMHLLNSPPMVLATLAFASSELALHLLNAVTLAVWYIARQIS 169
 181 RELFTVHSEVTVVAMHLLNSPPMVLATLAFASSELALHLLNAVTLAVWYIARQIS 303
 Q7 181 SGGQSRKLANMLLSHVRHA 201
 361 SGGQSRKLANMLLSHVRHA 384

RESULT 10

US-08-826-620A-7
 Sequence 7, Application US/08836620A
 Patent No. 5958710
 GENERAL INFORMATION:
 APPLICANT:
 TITLE OF INVENTION: Orphan receptor
 NUMBER OF SEQUENCES: 19
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC DOS/MS DOS
 SOFTWARE: Release #1.0, Version #1.25 (PFO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08-826-620A
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 62/076966/59333
 FILING DATE: 08-SEP-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GR 9518272.1
 FILING DATE: 08-SEP-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GR 9605550.4
 FILING DATE: 15-MAR-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GR 9607532.0
 FILING DATE: 11-APR-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GR 9609576.5
 FILING DATE: 08-MAY-1996
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 226 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 INFORMATION FOR SEQ ID NO: 7:
 ORIGIN: SOURCE:
 ORGANISM: Rattus rattus
 US-08-826-620A-7

Query Match: 79.9%; Score 944; DB 2; Length 226;
 Best Local Similarity: 93.4%; Prod. No. 1.6e-105;
 Matches: 183; Conservative: 6; Mismatches: 7; Indels: 0; Gaps: 0;

Q7 48 ELVHMLSAKFTDQVPSIFLVAVPIFSTWMPVIMWGIKMPSTIDQKILFAPDLVLD 97
 111 ELVHMLSAKFTDQVPSIFLVAVPIFSTWMPVIMWGIKMPSTIDQKILFAPDLVLD 156
 181 ELVHMLSAKFTDQVPSIFLVAVPIFSTWMPVIMWGIKMPSTIDQKILFAPDLVLD 303
 Q7 98 DQDFVCEVTLTFFMELTTSSEFTFLCEPPYLGVAMHLLNSMVTPLATGAGASIR 157
 41 DQDFVCEVTLTFFMELTTSSEFTFLCEPPYLGVAMHLLNSMVTPLATGAGASIR 316
 Q7 158 KVAHNAVIAAGVAVIAAGVAVIAAGVAVIAAGVAVIAAGVAVIAAGVAVIAAG 217

Q7 218 VVYVLLLEMLNAVHLL 233
 181 VVYVLLLEMLNAVHLL 196

RESULT 11

US-08-764-870-12
 Sequence 12, Application US/08764870
 Patent No. 635946
 GENERAL INFORMATION:
 APPLICANT: Scanlan, Thomas S
 APPLICANT: Baxter, John D
 APPLICANT: Fleiterick, Robert J
 APPLICANT: Wagner, Richard L
 APPLICANT: Kushner, Peter J
 APPLICANT: Aprilotti, James W
 TITLE OF INVENTION: Nuclear Receptor Ligands and Ligand
 TITLE OF INVENTION: Binding Domains
 NUMBER OF SEQUENCES: 16
 CORRESPONDENCE ADDRESS:
 ADDRESS: Cooley Godward
 STREET: Five Palo Alto Square, 3000 El Camino Real
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94306
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.10
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08-764/870
 FILING DATE: 11-DEC-1996
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/008,540
 FILING DATE: 13-DEC-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/008,543
 FILING DATE: 13-DEC-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/008,606
 FILING DATE: 14-DEC-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Nakamura, Jackie N
 REGISTRATION NUMBER: 35,966
 TELEPHONE: (650)843-5000
 TELEPHONE: (650)843-5000
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 595 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-764-870-12

Query Match: 64.3%; Score 759; DB 4; Length 595;
 Best Local Similarity: 60.2%; Prod. No. 1.4e-82;
 Matches: 142; Conservative: 54; Mismatches: 36; Indels: 4; Gaps: 3;

Q7 1 EVLLLEAVGVVLSR--PSNAFTFASMMMSILKALFEELVMTSWAKTQSPVETSL 68
 317 EVLLLEAVGVVLSR--PSNAFTFASMMMSILKALFEELVMTSWAKTQSPVETSL 126
 Q7 59 EVVLLLEAVGVVLSR--PSNAFTFASMMMSILKALFEELVMTSWAKTQSPVETSL 118

Sequence 14: Application US/08764870
Patent No. 6,266,446

PERSONAL INFORMATION:

APPLICANT: Scanlan, Thomas S

APPLICANT: Baxter, John D

APPLICANT: Fletcher, Robert J

APPLICANT: Wadner, Richard L

APPLICANT: Koshner, Peter J

APPLICANT: Apfelter, James W

APPLICANT: West, Brian

TITLE OF INVENTION: Nuclear Receptor Ligands and Ligand

TITLE OF INVENTION: Binding Domains

NUMBER OF SEQUENCES: 16

ADDRESSING ADDRESS:

ADDRESS: Cooley Goddard

STREET: Five Palo Alto Square, 3000 El Camino Real

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94306

SEQUENCE READABLE FORM:

COMPILED TYPE: floppy disk

OPERATING SYSTEM: PC 166/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.10

APPLICANT NUMBER: US 60/764,870

FILING DATE: 14-Dec-1996

CLASSIFICATION: 530

PREVIOUS APPLICATION DATA:

APPLICATION NUMBER: US 60/7008,540

FILING DATE: 14-Dec-1995

PREVIOUS APPLICATION DATA:

APPLICATION NUMBER: US 60/7008,543

FILING DATE: 14-Dec-1995

PREVIOUS APPLICATION DATA:

APPLICATION NUMBER: US 60/7008,546

FILING DATE: 14-Dec-1995

PREVIOUS APPLICATION DATA:

APPLICATION NUMBER: US 60/7008,549

FILING DATE: 14-Dec-1995

PREVIOUS APPLICATION DATA:

APPLICATION NUMBER: US 60/7008,550

FILING DATE: 14-Dec-1995

PREVIOUS APPLICATION DATA:

APPLICATION NUMBER: US 60/7008,551

FILING DATE: 14-Dec-1995

PREVIOUS APPLICATION DATA:

APPLICATION NUMBER: US 60/7008,552

FILING DATE: 14-Dec-1995

PREVIOUS APPLICATION DATA:

APPLICATION NUMBER: US 60/7008,553

FILING DATE: 14-Dec-1995

PREVIOUS APPLICATION DATA:

APPLICATION NUMBER: US 60/7008,554

FILING DATE: 14-Dec-1995

PREVIOUS APPLICATION DATA:

APPLICATION NUMBER: US 60/7008,555

FILING DATE: 14-Dec-1995

PREVIOUS APPLICATION DATA:

APPLICATION NUMBER: US 60/7008,556

FILING DATE: 14-Dec-1995

Search completed: July 12, 2002, 14:46:11
Job time: 119 sec

* * *

GenPro version 4.5
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Multi-Sequence Protein Search, using SW model

Run on: July 12, 2002, 14:44:12 / Search time 28.19 seconds

(without alignments)
221,970 Million cell updates/sec

Database: Protein sources

Sequence: 1 CAVSIOVASCHVWWSVPI

FASTA: CAVSIOVASCHVWWSVPI

Score and E-value: BLAST0062
Gapop 10.0 / Gapext 0.5

Score file: 284138 seqs, 96009434 residues

Total number of hits satisfying chosen parameters: 284138

Minimum DB seq length: 0
Maximum DB seq length: 20000000

Post processing: Minimum Match 0%

Maximum Match 100%

Listed first 45 summaries

Print No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Print No. | Score | Match | Length | DB | ID | Description |
|-----------|-------|-------|--------|----|---------|-------------------|
| 1 | 486 | 100.0 | 477 | 2 | S71400 | estrogen receptor |
| 2 | 486 | 100.0 | 503 | 2 | J080046 | estrogen receptor |
| 3 | 486 | 100.0 | 530 | 2 | J059339 | estrogen receptor |
| 4 | 484 | 99.2 | 586 | 1 | Q8XLE | estrogen receptor |
| 5 | 380 | 98.4 | 589 | 1 | Q8CHE | estrogen receptor |
| 6 | 480 | 98.4 | 595 | 1 | Q8HDE | estrogen receptor |
| 7 | 480 | 98.4 | 595 | 2 | I17110 | estrogen receptor |
| 8 | 480 | 98.4 | 599 | 1 | Q8MSE | estrogen receptor |
| 9 | 480 | 98.4 | 600 | 1 | Q8KLE | estrogen receptor |
| 10 | 480 | 98.4 | 620 | 2 | I10423 | estrogen receptor |
| 11 | 480 | 98.4 | 701 | 2 | S64737 | estrogen receptor |
| 12 | 480 | 98.4 | 724 | 2 | S64737 | estrogen receptor |
| 13 | 480 | 98.4 | 724 | 2 | S64737 | estrogen receptor |
| 14 | 480 | 98.4 | 724 | 2 | S64737 | estrogen receptor |
| 15 | 480 | 98.4 | 724 | 2 | S64737 | estrogen receptor |
| 16 | 480 | 98.4 | 724 | 2 | S64737 | estrogen receptor |
| 17 | 480 | 98.4 | 724 | 2 | S64737 | estrogen receptor |
| 18 | 480 | 98.4 | 724 | 2 | S64737 | estrogen receptor |
| 19 | 480 | 98.4 | 724 | 2 | S64737 | estrogen receptor |
| 20 | 480 | 98.4 | 724 | 2 | S64737 | estrogen receptor |
| 21 | 480 | 98.4 | 724 | 2 | S64737 | estrogen receptor |
| 22 | 480 | 98.4 | 724 | 2 | S64737 | estrogen receptor |
| 23 | 480 | 98.4 | 724 | 2 | S64737 | estrogen receptor |
| 24 | 480 | 98.4 | 724 | 2 | S64737 | estrogen receptor |
| 25 | 480 | 98.4 | 724 | 2 | S64737 | estrogen receptor |
| 26 | 480 | 98.4 | 724 | 2 | S64737 | estrogen receptor |
| 27 | 480 | 98.4 | 724 | 2 | S64737 | estrogen receptor |
| 28 | 480 | 98.4 | 724 | 2 | S64737 | estrogen receptor |
| 29 | 480 | 98.4 | 724 | 2 | S64737 | estrogen receptor |
| 30 | 480 | 98.4 | 724 | 2 | S64737 | estrogen receptor |

| | | | | | | |
|----|-----|------|-----|---|--------|--------------------|
| 30 | 242 | 60.1 | 923 | 2 | I54280 | progesterone recep |
| 31 | 242 | 60.1 | 930 | 2 | A25923 | progesterone recep |
| 32 | 242 | 60.1 | 933 | 1 | Q8HUP | progesterone recep |
| 33 | 242 | 60.1 | 981 | 2 | A41401 | progesterone recep |
| 34 | 242 | 60.1 | 984 | 2 | A29513 | progesterone recep |
| 35 | 241 | 59.8 | 450 | 2 | B47265 | progesterone recep |
| 36 | 241 | 59.8 | 452 | 2 | A36602 | progesterone recep |
| 37 | 227 | 52.3 | 763 | 1 | A25923 | progesterone recep |
| 38 | 226 | 58.5 | 443 | 1 | C36991 | progesterone recep |
| 39 | 226 | 58.5 | 447 | 2 | B34714 | progesterone recep |
| 40 | 226 | 58.5 | 454 | 2 | A36903 | progesterone recep |
| 41 | 226 | 58.5 | 454 | 2 | S06124 | progesterone recep |
| 42 | 226 | 58.5 | 458 | 2 | A44714 | progesterone recep |
| 43 | 226 | 58.5 | 469 | 2 | I11257 | progesterone recep |
| 44 | 224 | 58.0 | 389 | 2 | I49640 | progesterone recep |
| 45 | 224 | 58.0 | 390 | 2 | S44285 | progesterone recep |

ALIGNMENTS

RESULT 1

S71400

estrogen receptor beta human

C>Date: 29-Jan-1998 #sequence_revision 06 Feb 1998 #next change 20 Jan 2000

C/Accession: S71400

R/Mossmann, S.; Polman, J.; Dijkema, R.

FEBS Lett. 392: 49-53, 1996

A>Title: ER-beta: identification and characterization of a novel human estrogen recep

A/Reference number: S71400, MID:96454875

A/Accession: S71400

A/Molecule type: mRNA

A/Residues: 1-477 <M>

A/Cross reference: EMBL:K9101; NID:518262; PUB:CA6755.1; PUB:518263

C/Suprafamily: estrogen receptor; extra transforming protein; steroid binding; steroid hormone re

C/Keywords: DNA binding; nuclear phosphoprotein; steroid binding; steroid hormone re

E:94-97/Transl: extra transforming protein; steroid hormone re

E:96-116/Region: zinc finger motif

E:132-156/Region: zinc finger motif

E:167-182/Region: nuclear localization signal

E:22-24/Binding site: phosphate (Ser) (conserved) (by MAP kinase) #status predicted

E:56-79/113/116/Binding site: zinc (cys) #status predicted

F:132,138,148,151/Binding site: zinc (cys) #status predicted

Query Match

Best local similarity 100.0%; Score 386; DB 2; Length 477;

Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

db 1 CAVSIOVASCHVWWSVPIKAFKRSF728EYVPAIN;S1139H5555CA;P4K 60

db 96 CAVSIOVASCHVWWSVPIKAFKRSF728EYVPAIN;S1139H5555CA;P4K 155

db 61 CYEVM 66

db 156 CYEVM 161

RESULT 2

JM0046

estrogen receptor beta2 - rat

C/Accession: JM0046

C/Date: 17-Jun-1998 #sequence_revision 10-Jun 1998 #next change 17 Mar 1999

C/Species: Rattus norvegicus (Norway rat)

C/Accession: JM0046

C/Accession: JM0046

C/Accession: JM0046

Figure 1. Schematic representation of the experimental design. The subjects were divided into two groups: the control group (CG) and the experimental group (EG). The CG was divided into two subgroups: the control group (CG) and the experimental group (EG). The EG was divided into two subgroups: the control group (CG) and the experimental group (EG). The CG was divided into two subgroups: the control group (CG) and the experimental group (EG). The EG was divided into two subgroups: the control group (CG) and the experimental group (EG).

RESULT 21
A39248
androgen receptor - human
C1:Species: Homo sapiens (man)
C1Date: 04-sect-1991 #sequenced position 04-sect-1991
C1Accession: A39248; M0109; A00946; A4414; A2765; A0108; A4494; A2224

- [illegible]

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Multiple protein search, using SW model

Run on: July 12, 2002, 14:44:07, Search time 51.34 seconds
(without alignment)
142.791 Million cell updates/sec

Database: US-08-826-361a-3

Protein source: 1 CAVE-STAYASOTHEWAS-ET-AL-1998-1999-2000-2001-2002-2003-2004-2005-2006-2007-2008-2009-2010-2011-2012-2013-2014-2015-2016-2017-2018-2019-2020-2021-2022-2023-2024-2025-2026-2027-2028-2029-2030-2031-2032-2033-2034-2035-2036-2037-2038-2039-2040-2041-2042-2043-2044-2045-2046-2047-2048-2049-2050-2051-2052-2053-2054-2055-2056-2057-2058-2059-2060-2061-2062-2063-2064-2065-2066-2067-2068-2069-2070-2071-2072-2073-2074-2075-2076-2077-2078-2079-2080-2081-2082-2083-2084-2085-2086-2087-2088-2089-2090-2091-2092-2093-2094-2095-2096-2097-2098-2099-2100-2101-2102-2103-2104-2105-2106-2107-2108-2109-2110-2111-2112-2113-2114-2115-2116-2117-2118-2119-2120-2121-2122-2123-2124-2125-2126-2127-2128-2129-2130-2131-2132-2133-2134-2135-2136-2137-2138-2139-2140-2141-2142-2143-2144-2145-2146-2147-2148-2149-2150-2151-2152-2153-2154-2155-2156-2157-2158-2159-2160-2161-2162-2163-2164-2165-2166-2167-2168-2169-2170-2171-2172-2173-2174-2175-2176-2177-2178-2179-2180-2181-2182-2183-2184-2185-2186-2187-2188-2189-2190-2191-2192-2193-2194-2195-2196-2197-2198-2199-2200-2201-2202-2203-2204-2205-2206-2207-2208-2209-2210-2211-2212-2213-2214-2215-2216-2217-2218-2219-2220-2221-2222-2223-2224-2225-2226-2227-2228-2229-2230-2231-2232-2233-2234-2235-2236-2237-2238-2239-2240-2241-2242-2243-2244-2245-2246-2247-2248-2249-2250-2251-2252-2253-2254-2255-2256-2257-2258-2259-2260-2261-2262-2263-2264-2265-2266-2267-2268-2269-2270-2271-2272-2273-2274-2275-2276-2277-2278-2279-2280-2281-2282-2283-2284-2285-2286-2287-2288-2289-2290-2291-2292-2293-2294-2295-2296-2297-2298-2299-2300-2301-2302-2303-2304-2305-2306-2307-2308-2309-2310-2311-2312-2313-2314-2315-2316-2317-2318-2319-2320-2321-2322-2323-2324-2325-2326-2327-2328-2329-2330-2331-2332-2333-2334-2335-2336-2337-2338-2339-2340-2341-2342-2343-2344-2345-2346-2347-2348-2349-2350-2351-2352-2353-2354-2355-2356-2357-2358-2359-2360-2361-2362-2363-2364-2365-2366-2367-2368-2369-2370-2371-2372-2373-2374-2375-2376-2377-2378-2379-2380-2381-2382-2383-2384-2385-2386-2387-2388-2389-2390-2391-2392-2393-2394-2395-2396-2397-2398-2399-2400-2401-2402-2403-2404-2405-2406-2407-2408-2409-2410-2411-2412-2413-2414-2415-2416-2417-2418-2419-2420-2421-2422-2423-2424-2425-2426-2427-2428-2429-2430-2431-2432-2433-2434-2435-2436-2437-2438-2439-2440-2441-2442-2443-2444-2445-2446-2447-2448-2449-2450-2451-2452-2453-2454-2455-2456-2457-2458-2459-2460-2461-2462-2463-2464-2465-2466-2467-2468-2469-2470-2471-2472-2473-2474-2475-2476-2477-2478-2479-2480-2481-2482-2483-2484-2485-2486-2487-2488-2489-2490-2491-2492-2493-2494-2495-2496-2497-2498-2499-2500-2501-2502-2503-2504-2505-2506-2507-2508-2509-2510-2511-2512-2513-2514-2515-2516-2517-2518-2519-2520-2521-2522-2523-2524-2525-2526-2527-2528-2529-2530-2531-2532-2533-2534-2535-2536-2537-2538-2539-2540-2541-2542-2543-2544-2545-2546-2547-2548-2549-2550-2551-2552-2553-2554-2555-2556-2557-2558-2559-2560-2561-2562-2563-2564-2565-2566-2567-2568-2569-2570-2571-2572-2573-2574-2575-2576-2577-2578-2579-2580-2581-2582-2583-2584-2585-2586-2587-2588-2589-2590-2591-2592-2593-2594-2595-2596-2597-2598-2599-2600-2601-2602-2603-2604-2605-2606-2607-2608-2609-2610-2611-2612-2613-2614-2615-2616-2617-2618-2619-2620-2621-2622-2623-2624-2625-2626-2627-2628-2629-2630-2631-2632-2633-2634-2635-2636-2637-2638-2639-2640-2641-2642-2643-2644-2645-2646-2647-2648-2649-2650-2651-2652-2653-2654-2655-2656-2657-2658-2659-2660-2661-2662-2663-2664-2665-2666-2667-2668-2669-2670-2671-2672-2673-2674-2675-2676-2677-2678-2679-2680-2681-2682-2683-2684-2685-2686-2687-2688-2689-2690-2691-2692-2693-2694-2695-2696-2697-2698-2699-2700-2701-2702-2703-2704-2705-2706-2707-2708-2709-2710-2711-2712-2713-2714-2715-2716-2717-2718-2719-2720-2721-2722-2723-2724-2725-2726-2727-2728-2729-2730-2731-2732-2733-2734-2735-2736-2737-2738-2739-2740-2741-2742-2743-2744-2745-2746-2747-2748-2749-2750-2751-2752-2753-2754-2755-2756-2757-2758-2759-2760-2761-2762-2763-2764-2765-2766-2767-2768-2769-2770-2771-2772-2773-2774-2775-2776-2777-2778-2779-2780-2781-2782-2783-2784-2785-2786-2787-2788-2789-2790-2791-2792-2793-2794-2795-2796-2797-2798-2799-2800-2801-2802-2803-2804-2805-2806-2807-2808-2809-2810-2811-2812-2813-2814-2815-2816-2817-2818-2819-2820-2821-2822-2823-2824-2825-2826-2827-2828-2829-2830-2831-2832-2833-2834-2835-2836-2837-2838-2839-2840-2841-2842-2843-2844-2845-2846-2847-2848-2849-2850-2851-2852-2853-2854-2855-2856-2857-2858-2859-2860-2861-2862-2863-2864-2865-2866-2867-2868-2869-2870-2871-2872-2873-2874-2875-2876-2877-2878-2879-2880-2881-2882-2883-2884-2885-2886-2887-2888-2889-2890-2891-2892-2893-2894-2895-2896-2897-2898-2899-2900-2901-2902-2903-2904-2905-2906-2907-2908-2909-2910-2911-2912-2913-2914-2915-2916-2917-2918-2919-2920-2921-2922-2923-2924-2925-2926-2927-2928-2929-2930-2931-2932-2933-2934-2935-2936-2937-2938-2939-2940-2941-2942-2943-2944-2945-2946-2947-2948-2949-2950-2951-2952-2953-2954-2955-2956-2957-2958-2959-2960-2961-2962-2963-2964-2965-2966-2967-2968-2969-2970-2971-2972-2973-2974-2975-2976-2977-2978-2979-2980-2981-2982-2983-2984-2985-2986-2987-2988-2989-2990-2991-2992-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27 61 CYEWM 66
111111
28 156 CYEWM 161

RESULT 4

AAW31946
10 AAW31946 standard; Protein: 474 AA.

AA AAW31946.

10 23-JUN-2000 (first entry)

XX bovine ER-beta protein.

XX bovine ER-beta; estrogen receptor beta; anticancer anti-osteoporosis;

KW transcriptional transactivator; estrogen-dependent transcription; cancer;

KW estrogen-response element; ovary; prostate; osteoporosis

XX bovine ER-beta.

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ID AAW33212 standard; Protein: 477 AA.

AC AAW33212.

XX 20-APR-1998 (first entry)

XX human estrogen receptor protein.

XX estrogen receptor protein; steroid; alternative splicing; estradiol;

KW estrone; estradiol; screening.

XX Homo sapiens.

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RESULT 6

AAW14724
10 AAW14724 standard; Protein: 485 AA.

AC AAW14724.

XX 08-JUN-1997 (first entry)

XX human estrogen receptor beta (ER-beta).

XX orphan receptor; estrogen receptor beta; ER-beta;

KW nuclear receptor; prostate cancer; benign prostatic hyperplasia;

KW ovary cancer; cardiovascular disease; osteoporosis;

KW environment; pollutant.

XX Homo sapiens.

XX Homo sapiens.

[illegible]

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| TN | WP9911766 AL. |
| XX | |
| FD | 11 MAR-1999. |
| XX | |
| FF | 41 AUG-1998; 98W0 0818040. |
| XX | |
| FR | 04 SEP-1997; 9708-0924708. |
| XX | |
| FA | (HEBIC) UNIV CALIFORNIA. |
| XX | |
| FJ | constatsson J; Kulper abim; Kustner TJ; Nilsson S; |
| FJ | Porch K; Scandinavian IS; Webb P; |
| XX | |
| DR | WPI: 1999 205173/17. |
| DH | N ESDR: AAX26486. |
| XX | |
| FI | Screening for test compounds which inhibit or activate estrogen |
| FJ | receptor beta (ER beta) mediated activation at a Api site. For use |
| PT | in therapy |
| XX | |
| FS | claim 14; page 43-44; 61pp; English. |
| XX | |
| GC | The present sequence represents an estrogen receptor beta. The |
| GC | spectification describes a method for screening test compounds for |
| CC | differential estrogen receptor (ER) alpha mediated and ER beta mediated |
| CC | activation at an Api site. The method is used for identifying compounds |
| GC | which can be used in therapy. |
| XX | |
| SO | Sequence 485 AA: |
|
 | |
| Query Match | 100.0%; Score ABG: 18.20; Length 485; |
| Best Local Similarity | 100.0%; Prod. No. 4,796 44; |
| Matches | 662 Conservative 0; Mismatches 0; Indels 0; Gaps 0; |
|
 | |
| Q7 | I : CAAGTGGAAATGAACAGCTCAATTTTCGTGCGAATCATAGCTTGCTGGTGGTCAATGATGAG |
| LD | TT |
| QY | 61 CYEWM 66 |
| | TTTTTT |
| DH | 164 CYEGQM 169 |
|
 | |
| RESIDU 8 | |
| AAMK3215 | |
| ID | AAMK3215 standard; protein; 540 AA. |
| XX | |
| AI | AAMK3215; |
| XX | |
| IE | 20 APR 1998 (FIRST ENTRY) |
| XX | |
| DE | HUMAN OSTROGEN RECEPTOR PROTEIN #2. |
| XX | |
| KW | ESTROGEN RECEPTOR PROTEIN; STEROID; ALTERNATIVE SPLICING; ESTRADOL; |
| RW | OSTROGEN; OSTROL; SCREENING. |
| XX | |
| CS | HOMO SAPIDUS. |
| XX | |
| FN | E0798378 A2. |
| XX | |
| PD | 01 OCT 1997. |
| XX | |
| PE | 25-MAR-1997; 97EP 0200903. |
| XX | |
| PR | 22-NV-1996; 96EP 0204884. |
| XX | |
| PR | 26-MAR 1996; 96EP 0200820. |
| XX | |
| TA | (AUK) J ARKO N BELL NV. |
| XX | |
| TI | 01/KOMA R.; MOSELMAN SE |
| XX | |
| WR | WPI: 1997 474189/44. |

DB 125 CEEVEM 140

RESULT 2

US-08-846-620A 4

Sequence 14, Application US/08846620A

Patient No. 9958710

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: orphan receptor

NUMBER OF SEQUENCES: 19

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patient In Release #1.0, Version #1.25 (EPO)

SEQUENCE APPLICATION DATA:

APPLICATION NUMBER: 05/98/846,620A

FILING DATE:

Prior Application DATA:

APPLICATION NUMBER: PCT/EP96/03933

FILING DATE:

APPLICATION NUMBER: GB 9518272.1

FILING DATE: 08 SEP 1995

Prior Application NUMBER:

APPLICATION NUMBER: GB 9605550.4

FILING DATE: 15 MAR 1996

Prior Application DATA:

APPLICATION NUMBER: GB 9607542.0

FILING DATE: 11 APR 1996

Prior Application DATA:

APPLICATION NUMBER: GB 9609576.5

FILING DATE: 08 MAY 1996

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 485 amino acids

TYPE: amino acid

TOPOLOGY: linear

ORGANISM: Homo sapiens

US-08-846-620A 4

Query Match 100.0% Score 4862 DB 22 Length 4852

Best Local Similarity 100.0% Pctd. No. 7,80-472

Matches 667 Conserved 02 Mismatches 02 Indels 02 Caps 02

DB 104 CAVSLSVASYGVYVWSSDRAKAFKRSIGGNLYPTVATNCTTDRKRSYVA*GLAR 60

UY 61 CEEVEM 66

DB 164 CEEVEM 169

RESULT 3

US-09-149-617 1

Sequence 14, Application US/09149617

Patient No. 6222015

GENERAL INFORMATION:

APPLICANT: WILKINSON, HILARY

TITLE OF INVENTION: ESTROGEN RECEPTOR

FILE REFERENCE: 230477

CURRENT APPLICATION NUMBER: 05/97/09,617

CURRENT FILING DATE: 1998-08-25

EARLIER APPLICATION NUMBER: 62/298,271

EARLIER FILING DATE: 1997-09-08

EARLIER APPLICATION NUMBER: 62/298,270

EARLIER FILING DATE: 1997-09-08

NUMBER OF SEQ ID NOS: 22

SOFTWARE: FastSeq for Windows Version 3.0

LENGTH: 548

TYPE: PCT

ORGANISM: HUMAN

US-09-149-617-1

Query Match 100.0% Score 4862 DB 22 Length 5482

Best Local Similarity 100.0% Pctd. No. 8,90-472

Matches 667 Conserved 02 Mismatches 02 Indels 02 Caps 02

DB 104 CAVSLSVASYGVYVWSSDRAKAFKRSIGGNLYPTVATNCTTDRKRSYVA*GLAR 60

UY 61 CEEVEM 66

DB 164 CEEVEM 169

RESULT 4

US-08-846-620A-14

Sequence 14, Application US/08846620A

Patient No. 9958710

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: orphan receptor

NUMBER OF SEQUENCES: 19

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patient In Release #1.0, Version #1.25 (EPO)

SEQUENCE APPLICATION DATA:

APPLICATION NUMBER: 05/98/846,620A

FILING DATE:

Prior Application DATA:

APPLICATION NUMBER: PCT/EP96/03933

FILING DATE:

APPLICATION NUMBER: GB 9518272.1

FILING DATE: 08-SEP-1995

Prior Application DATA:

APPLICATION NUMBER: GB 9605550.4

FILING DATE: 15 MAR 1996

Prior Application DATA:

APPLICATION NUMBER: GB 9609576.5

FILING DATE: 08 MAY 1996

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 484 amino acids

TYPE: amino acid

TOPOLOGY: linear

ORGANISM: Mus musculus

US-08-846-620A-14

Query Match 99.2% Score 4842 DB 22 Length 4842

Best Local Similarity 98.5% Pctd. No. 1,70-402

Matches 657 Conserved 12 Mismatches 02 Indels 02 Caps 02

DB 104 CAVSLSVASYGVYVWSSDRAKAFKRSIGGNLYPTVATNCTTDRKRSYVA*GLAR 60

UY 61 CEEVEM 66

DB 164 CEEVEM 169

RESULT 5

US-08-846-620A-5
Sequence 5, Application US/08836620A
Patent No. 5958710
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: orphan receptor
NUMBER OF SEQUENCES: 19
MEDIUM READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08-846-620A
FILING DATE:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/009033
FILING DATE:
APPLICATION NUMBER: GB 9518272.1
FILING DATE:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: GB 9605550.4
FILING DATE: 15-MAR-1996
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: GB 9607532.0
FILING DATE: 11-APR-1996
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: GB 9609576.5
FILING DATE: 08-MAY-1996
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 485 amino acids
TYPE: amino acid
TOPOLOGY: linear
ORIGINAL SOURCE:
ORGANISM: Mus musculus
US-08-846-620A-5

Query Match 99.28; Score 383; DB 2; Length 485;
Best Local Similarity 98.58; Pred. No. 1,76-36;
Matches 65; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAVSDVASTVHYVWWSCTPKAFKRSISGHNTYTPALNCTIDKNNPKSCVAATLKK 60
DB 104 CAVSDVASTVHYVWWSCTPKAFKRSISGHNTYTPALNCTIDKNNPKSCVAATLKK 163

QY 61 CYEWGM 66
DB 164 CYEWGM 169

RESULT 6
US-08-846-620A-11
Sequence 11, Application US/08836620A
Patent No. 5958710
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: orphan receptor
NUMBER OF SEQUENCES: 19
MEDIUM READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08-846-620A
FILING DATE:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/009033
FILING DATE:
APPLICATION NUMBER: GB 9518272.1
FILING DATE:
APPLICATION NUMBER: GB 9605550.4
FILING DATE: 15-MAR-1996
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: GB 9607532.0
FILING DATE: 11-APR-1996
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: GB 9609576.5
FILING DATE: 08-MAY-1996
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 484 amino acids
TYPE: amino acid
TOPOLOGY: linear
ORIGINAL SOURCE:
ORGANISM: Rattus rattus
US-08-846-620A-13

PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9605550.4
FILING DATE: 15-MAR-1996
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: GB 9607532.0
FILING DATE: 11-APR-1996
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: GB 9609576.5
FILING DATE: 08-MAY-1996
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 66 amino acids
TYPE: amino acid
TOPOLOGY: linear
ORIGINAL SOURCE:
ORGANISM: Rattus rattus
US-08-846-620A-11

Query Match 98.78; Score 381; DB 2; Length 66;
Best Local Similarity 98.58; Pred. No. 3,56-37;
Matches 65; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAVSDVASTVHYVWWSCTPKAFKRSISGHNTYTPALNCTIDKNNPKSCVAATLKK 60
DB 1 CAVSDVASTVHYVWWSCTPKAFKRSISGHNTYTPALNCTIDKNNPKSCVAATLKK 60

QY 61 CYEWGM 66
DB 61 CYEWGM 66

RESULT 7
US-08-836-620A-13
Sequence 13, Application US/08836620A
Patent No. 5958710
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Orphan receptor
NUMBER OF SEQUENCES: 19
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08-836-620A
FILING DATE:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/03933
FILING DATE:
APPLICATION NUMBER: GB 9518272.1
FILING DATE: 08-SEP-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: GB 9605550.4
FILING DATE: 15-MAR-1996
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: GB 9607532.0
FILING DATE: 11-APR-1996
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: GB 9609576.5
FILING DATE: 08-MAY-1996
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 484 amino acids
TYPE: amino acid
TOPOLOGY: linear
ORIGINAL SOURCE:
ORGANISM: Rattus rattus
US-08-846-620A-13

Query Match 98.78; Score 381; DB 2; Length 484;


```

RESULT 11
US-08-826-620A-17
Sequence 17: Application US/08836620A
Patent No. 5962710
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Orphan receptor
NUMBER OF SEQUENCES: 19
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC/MS DOS
TELECOMMUNICATION INFORMATION:
FILING DATE:
TELEFAX: (619) 535-7001
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08836620A
FILING DATE:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/01034
FILING DATE:
APPLICATION NUMBER: US 9518272.1
FILING DATE: 08-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 9605550.4
FILING DATE: 15-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 9607542.0
FILING DATE: 11-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 9607542.0
FILING DATE: 11-APR-1996
SEQUENCE CHARACTERISTICS:
LENGTH: 591 amino acids
TYPE: amino acid
TOPOLOGY: linear
ORGANISM: Homo sapiens
US-08-826-620A-17

Query Match          98.4% Score 380; DB 2; Length 591;
Post Local Similarity 97.0% Prod. No. 4 Re-16;
Matches 64; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

CY 1 CAVSDASVYHWVWSTFKATFSTGHRATPATVSTTKRKRKSGATRR 60
DB 185 CAVNDASVYHWVWSTFKATFSTGHRATPATVSTTKRKRKSGATRR 244

CY 61 CYEVM 66
DB 245 CYEVM 250

```

```

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/041,886
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 41,815
REFERENCE/DOCKET NUMBER: P-LT 2626
TELECOMMUNICATION INFORMATION:
FILING DATE:
TELEFAX: (619) 535-7001
INFORMATION FOR SFO ID NO: 35;
SEQUENCE CHARACTERISTICS:
LENGTH: 595 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-041-886-35

Query Match          98.4% Score 380; DB 4; Length 595;
Post Local Similarity 97.0% Prod. No. 4 Re-16;
Matches 64; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

CY 1 CAVSDASVYHWVWSTFKATFSTGHRATPATVSTTKRKRKSGATRR 60
DB 185 CAVNDASVYHWVWSTFKATFSTGHRATPATVSTTKRKRKSGATRR 244

CY 61 CYEVM 66
DB 245 CYEVM 250

RESULT 13
US-08-764-870-12
Sequence 12: Application US/087644870
Patent No. 6236946
GENERAL INFORMATION:
APPLICANT: Scanlan, Thomas S
APPLICANT: Baxter, John D
APPLICANT: Fletcher, Robert J
APPLICANT: Wagner, Richard L
APPLICANT: Kuchner, Peter J
APPLICANT: Apriletti, James W
APPLICANT: West, Brian
TITLE OF INVENTION: Nuclear Receptor ligands and ligand
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooley Goddard
STREET: Five Palo Alto Square, 3000 El Camino Real
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC/MS DOS
SOFTWARE: Patent release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/087644870
FILING DATE: 13-DEC-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/008,540
FILING DATE: 13-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/008,543
FILING DATE: 13-DEC-1995
PRIOR APPLICATION DATA:

```


| | | | |
|----|-----|-----------|-----|
| LY | 61 | CYEVGM | 66 |
| | | 1 : 1 1 1 | |
| LD | 153 | CIRVGM | 168 |

; CURRENT APPLICATION NUMBER: 18/09/500
 ; CURRENT FILING DATE: 200-02-09
 ; PARTIAL APPLICATION NUMBER: 9705451.4

```

1 EAVLIER FILING DATE: 1997-04-17
2 EAVLIER APPLICATION NUMBER: 9804289.9
3 EAVLIER FILING DATE: 1996-02-16
4 NUMBER OF SEQ TO NOS: 4
5 SOFTWARE: FASTSEQ FOR WINDOWS Version 4.0
6 SEQ ID NO: 2
7 LENGTH: 435
8 TYPE: PRT
9 ORGANISM: Homo sapiens
10 US 09-141-000 2

```

Query Match 71.5% Score 276; DB 4; Length 435;

Best Local Similarity 72.7% Prod. No. 4,76-24;

Matches 48; Consol val 19; 5; Mismatches 14; Indels 0; Gaps 0;

```

1 1 GAVSNVASYVYGVWSVYDPAERKESVQDINQVVAHQVTLQRRKRSVQVRLK 60
2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
3 103 GVVQDASHYGVASVQVAKPKRIQVIMVSVVAMRDELKESKSVQVRLK 104

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Query 64 CYEVM 66

DB 165 CLKVM 170

RESULT 20

US 09-141-000 4

Sequence 4; Application US/09141000

Patent No. 6024295

GENERAL INFORMATION:

APPLICANT: Chem. Pat.

TITLE OF INVENTION: DNA POLYMERASE EXPRESSION HUMAN NUTRIAR

TITLE OF INVENTION: POLYMERASE

FILE REFERENCE: 199909

CURRENT APPLICATION NUMBER: US/09/141-000

PRIOR FILING DATE: 1998-09-26

NUMBER OF SEQ TO NOS: 40

SOFTWARE: FASTSEQ FOR WINDOWS Version 4.0

SEQ ID NO: 4

LENGTH: 458

TYPE: PRT

ORGANISM: Human

US 09-141-000 4

Query Match 71.5% Score 276; DB 4; Length 458;

Best Local Similarity 72.7% Prod. No. 4,76-24;

Matches 48; Consol val 19; 5; Mismatches 13; Indels 0; Gaps 0;

```

1 1 GAVSNVASYVYGVWSVYDPAERKESVQDINQVVAHQVTLQRRKRSVQVRLK 60
2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
3 103 GVVQDASHYGVASVQVAKPKRIQVIMVSVVAMRDELKESKSVQVRLK 104

```

Query 64 CYEVM 66

DB 165 CLKVM 170

RESULT 21

US 09-141-000 2

Sequence 2; Application US/09141000

Patent No. 6024295

GENERAL INFORMATION:

APPLICANT: Chem. Pat.

TITLE OF INVENTION: DNA POLYMERASE EXPRESSION HUMAN NUTRIAR

TITLE OF INVENTION: POLYMERASE

FILE REFERENCE: 199909

CURRENT APPLICATION NUMBER: US/09/141-000

PRIOR FILING DATE: 1998-09-26

NUMBER OF SEQ TO NOS: 40

SOFTWARE: FASTSEQ FOR WINDOWS Version 4.0

SEQ ID NO: 2

LENGTH: 500

```

1 TYPE: PRT
2 ORGANISM: Human
3 US-09-141-000 2

```

Query Match 71.5% Score 276; DB 4; Length 500;

Best Local Similarity 72.7% Prod. No. 4,76-24;

Matches 48; Consol val 19; 5; Mismatches 14; Indels 0; Gaps 0;

```

1 1 GAVSNVASYVYGVWSVYDPAERKESVQDINQVVAHQVTLQRRKRSVQVRLK 60
2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
3 103 GVVQDASHYGVASVQVAKPKRIQVIMVSVVAMRDELKESKSVQVRLK 104

```

Query 64 CYEVM 66

DB 165 CLKVM 168

RESULT 22

US-08-846-620A 18

Sequence 18; Application US/08846620A

Patent No. 5958710

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: orphan receptor

NUMBER OF SEQUENCES: 19

COMPUTER RELEVABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC DOS/MS DOS

SOFTWARE: Patent to Release #1.0, Version #1.25 (2000)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/846-620A

PRIOR FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/846-620A

PRIOR FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/846-620A

PRIOR FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/846-620A

PRIOR FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/846-620A

PRIOR FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/846-620A

PRIOR FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/846-620A

PRIOR FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/846-620A

PRIOR FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/846-620A

PRIOR FILING DATE:

REGISTRATION NUMBER: 41,015
 REFERENCE/AGENT NUMBER: P-1 2626
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 546-9001
 TELEFAX: (619) 546-9049
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 918 amino acids
 TYPE: amino acid
 PRIMARY: linear
 MOLECULE TYPE: protein
 DS: 08-087-151-11

Query Match: 61.1% Score: 289; ID: 4; Length: 918
 Best Local Similarity: 59.1% Prod. No. 1, 60-19; Indels: 0; Gaps: 0
 Matches: 592 Conserved: 92; Mismatches: 18; Indels: 0; Gaps: 0

57 1 CAWSSYASVYGVWSYVKAATKSTGQINDYDQATNGLDNGKRSVAVRQK 60
 1 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 10 508 CLGQASRQYGVGLDQSGVFKKAVKSGYVAVSNLTDQKSPKTSVQK 617
 57 61 GYEVAM 66
 10 619 GYEVAM 624

RESULT: 26
 5/17/02 1
 Patent No. 5,217,967
 APPLICANT: EVANGELINE M. NAZARETH, N. NAZARETH, STANLEY M.
 TITLE OF INVENTION: RECEPTOR LIGAND IDENTIFICATION,
 CHARACTERIZATION, IDENTIFICATION AND USE
 NUMBER OF SEQUENCES: 4
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 08/072,278, 614
 FILING DATE: 09 NOV 1994
 SEQ ID NO: 1
 LENGTH: 66
 5/17/02 1

Query Match: 61.1% Score: 289; ID: 6; Length: 66
 Best Local Similarity: 59.1% Prod. No. 1, 70-20; Indels: 0; Gaps: 0
 Matches: 592 Conserved: 92; Mismatches: 18; Indels: 0; Gaps: 0

57 1 CAWSSYASVYGVWSYVKAATKSTGQINDYDQATNGLDNGKRSVAVRQK 60
 1 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 10 1 CWSYASRQYGVGLDQSGVFKKAVKSGYVAVSNLTDQKSPKTSVQK 69
 57 61 GYEVAM 66
 10 619 GYEVAM 624

RESULT: 27
 DS: 08-087-151-1
 Sequence: 4, Application US/0807151
 Patent No. 5,468,624
 GENERAL INFORMATION:
 APPLICANT: E. Brad Thompson
 APPLICANT: Lyne V. Nazareth
 TITLE OF INVENTION: ACTIVITY OF A REGULATED FRAGMENT
 NUMBER OF SEQUENCES: 4
 CLASSIFICATION: 540
 ADDRESS/AGENT ADDRESS:
 ADDRESS: Arnold, White & Burke
 STREET: P.O. Box 4434
 CITY: Houston
 STATE: Texas
 COUNTRY: USA
 ZIP: 77210
 COMPUTER READABLE FORM:
 5/17/02 1

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: pc dos/MS DOS
 SOFTWARE: WordPerfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 08/087,151
 FILING DATE: July 7, 1994
 CLASSIFICATION: 435
 ADDRESS/AGENT INFORMATION:
 NAME: Hodgins, Daniel S.
 REGISTRATION NUMBER: 41,026
 REFERENCE/AGENT NUMBER: 01-01,141/100
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 512-320-7200
 TELEFAX: 512-474-7577
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 89 amino acid residues
 TYPE: amino acid
 PRIMARY: single
 MOLECULE TYPE: peptide
 DS: 08-087-151-3

Query Match: 61.1% Score: 289; ID: 1; Length: 89
 Best Local Similarity: 59.1% Prod. No. 2, 30-20; Indels: 0; Gaps: 0
 Matches: 592 Conserved: 92; Mismatches: 18; Indels: 0; Gaps: 0

57 1 CAWSSYASVYGVWSYVKAATKSTGQINDYDQATNGLDNGKRSVAVRQK 60
 1 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 10 2 CWSYASRQYGVGLDQSGVFKKAVKSGYVAVSNLTDQKSPKTSVQK 89
 57 61 GYEVAM 66
 10 84 CWSYAM 89

RESULT: 28
 DS: 08-087-151-3
 Sequence: 4, Application US/0861072
 Patent No. 5,571,791
 GENERAL INFORMATION:
 APPLICANT: E. Brad Thompson
 APPLICANT: Lyne V. Nazareth
 TITLE OF INVENTION: ACTIVITY OF A REGULATED FRAGMENT
 NUMBER OF SEQUENCES: 4
 ADDRESS/AGENT ADDRESS:
 ADDRESS: Arnold, White & Burke
 STREET: P.O. Box 4434
 CITY: Houston
 STATE: Texas
 COUNTRY: USA
 ZIP: 77210
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: pc dos/MS DOS
 SOFTWARE: WordPerfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 08/087,151
 FILING DATE: July 7, 1994
 CLASSIFICATION: 435
 ADDRESS/AGENT INFORMATION:
 NAME: Hodgins, Daniel S.
 REGISTRATION NUMBER: 41,026
 REFERENCE/AGENT NUMBER: 01-01,141/100
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 512-320-7200
 TELEFAX: 512-474-7577
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 89 amino acid residues
 TYPE: amino acid
 PRIMARY: single
 MOLECULE TYPE: peptide
 DS: 08-087-151-3

...

439 CATTLESM FV MGT WPS HOPKIL FAQNT 11 DPNEEDVEYOMI NIFMULATASP 438

Query Match: 59.3%; Score 700; Pk: 2; Length 701;

Accession: F00044

Receptor, beta, M-type, beta-2-adrenergic, Pheox, K., Mowbray, J.B., Jones, S.A., Baring, E.L., 94

Receptor, beta-2-adrenergic, Pheox, K., Mowbray, J.B., Jones, S.A., Baring, E.L., 94

Accession: F00044; M01070800286

Accession: F00044

Accession: F00044

Accession: F00044; M01070800286

Query Match

Query Match 21.7% Score 254; 108.2; Length 80;

Best Local Similarity 100.0%; Prod. No. 1.3e-162

Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 20

Protein: 20

Accession: F00044; M01070800286

Accession: F00044; M01070800286

Accession: F00044; M01070800286

Accession: F00044; M01070800286

Accession: F00044; M01070800286

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Accession: F00044; M01070800286

Accession: F00044; M01070800286

Accession: F00044; M01070800286

A: Acetone solution: 550/50
A: Solvent: propanol

C:\Bible: 13 Jul 1996, #sequence, revision 13 Jul 1996, #vol, change 20 Aug 1999
 C:\Accession: S2669, 16460

R. Manteufelskott, D. J., Boronovoyt, H., Heymann, R. A., Zhou, J. Y., and, E. S., 1999, A. E., R. G. Jones [wev, 6, 429-444, 1992

